

Result No.	Query			Description	
	Score	Match	Length	ID	
1	5961	100.0	1132	9	US-09-990-080-2
2	5961	100.0	1132	9	US-09-749-728B-31
3	5961	100.0	1132	9	US-09-843-676-225
4	5961	100.0	1132	9	US-09-953-052-2
5	5961	100.0	1132	11	US-09-788-110A-23
6	5961	100.0	1132	14	US-10-053-758-225
7	5961	100.0	1132	14	US-10-208-243-2
8	5961	100.0	1132	14	US-10-054-295-225
9	5961	100.0	1132	14	US-10-054-611-225
10	5961	100.0	1132	14	US-10-105-963-2
11	5961	100.0	1132	14	US-10-044-592-2
12	5961	100.0	1132	14	US-10-044-539-2
13	5961	100.0	1132	14	US-10-295-681-57
					Sequence 2, Appli
					Sequence 31, Appl
					Sequence 225, App
					Sequence 2, Appli
					Sequence 23, Appl
					Sequence 225, App
					Sequence 2, Appli
					Sequence 225, App
					Sequence 225, App
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 57, Appl

QY 181 ATQARPPPHASGPRRLRGCEAWNHSVREAGVPLGLPAPGARRGGASRSRLPLPKPRR 240  
DB 181 ATQARPPPHASGPRRLRGCEAWNHSVREAGVPLGLPAPGARRGGASRSRLPLPKPRR 240  
QY 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEBATSLEGALSCTRSHSPSVG 300  
DB 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEBATSLEGALSCTRSHSPSVG 300  
QY 301 RQHHAGPSTSRPPRPWDTPCPVVAETKHFVLSGDKQELRPSFLSSRPSLTGARRL 360  
DB 301 RQHHAGPSTSRPPRPWDTPCPVVAETKHFVLSGDKQELRPSFLSSRPSLTGARRL 360  
QY 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCYPGVLLKTHCPRAAVT 420  
DB 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCYPGVLLKTHCPRAAVT 420  
QY 421 PAAGVCAREKQGSVAAPPEEDTDPRLVQLLRQHSSPWQYVGFVRACLRRLVPPGLWGS 480  
DB 421 PAAGVCAREKQGSVAAPPEEDTDPRLVQLLRQHSSPWQYVGFVRACLRRLVPPGLWGS 480  
QY 481 RHNERRFLRNTKKFISLGKHAKLSIQLTWMKSVRDCAWLRSPGVCVPAAEHRLREI 540  
DB 481 RHNERRFLRNTKKFISLGKHAKLSIQLTWMKSVRDCAWLRSPGVCVPAAEHRLREI 540  
QY 541 LAKFLHMLMSYVVELLRSPFYVTETTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVOLRE 600  
DB 541 LAKFLHMLMSYVVELLRSPFYVTETTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVOLRE 600  
QY 601 LSEAEVQHRREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660  
DB 601 LSEAEVQHRREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660  
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLRVRAODPPPELVFKVDVTGAYDTI 720  
DB 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLRVRAODPPPELVFKVDVTGAYDTI 720  
QY 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780  
DB 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780  
QY 781 QETSPLRDVAIVIEOSSLINEASSGLFDVFLRPMCHHAVIRGKSYVQCQGIPOGSIILSTL 840  
DB 781 QETSPLRDVAIVIEOSSLINEASSGLFDVFLRPMCHHAVIRGKSYVQCQGIPOGSIILSTL 840  
QY 841 LCSICYGDMENKLFAGIRRDGLLRLVDDFLLVTHLTHAKTFLRTLVRGVPYGCVMNL 900  
DB 841 LCSICYGDMENKLFAGIRRDGLLRLVDDFLLVTHLTHAKTFLRTLVRGVPYGCVMNL 900  
QY 901 RKTVNPVBEALGGTAFVQMPAHGLFPWCGLLDTRTLLEVQSDYSSYARTSIRASLTF 960  
DB 901 RKTVNPVBEALGGTAFVQMPAHGLFPWCGLLDTRTLLEVQSDYSSYARTSIRASLTF 960  
QY 961 NRGFKAGNRMRKLFGLVRLKCHSLFDLDQVNSLQVCTNIIYKILLQAYRHACVLQLP 1020  
DB 961 NRGFKAGNRMRKLFGLVRLKCHSLFDLDQVNSLQVCTNIIYKILLQAYRHACVLQLP 1020  
QY 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080  
DB 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080  
QY 1081 KLTRHRVTVYVPLLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132  
DB 1081 KLTRHRVTVYVPLLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132

RESULT 2

US-09-749-728B-31

; Sequence 31, Application US/09749728B  
; Patent No. US20020142457A1  
; GENERAL INFORMATION:  
; APPLICANT: Umezawa, Akihiro  
; APPLICANT: Hata, Jun-ichi

; APPLICANT: Fukuda, Keiichi  
; APPLICANT: Ogawa, Satoshi  
; APPLICANT: Sakurada, Kazuhiro  
; APPLICANT: Gojo, Satoshi  
; APPLICANT: Yamada, Yoji  
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOM  
; FILE REFERENCE: 00766.000043  
; CURRENT APPLICATION NUMBER: US/09/749, 728B  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: H11-372826  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: PCT-JP00-011148  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: PCT-JP00-07741  
; PRIOR FILING DATE: 2000-11-02  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn Ver.2.0  
; SEQ ID NO 31  
; LENGTH: 1132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-749-728B-31

Query Match 100.0%; Score 5961; DB 9; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60  
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DB 61 DARPPAAPSPFQVSCLELKVAVLQRLCERGAKNVLAFGPALLDGARGGPEAFTTSVR 120  
QY 121 SYLPTNTVDALRGSAWGALLRRVGGDVLVHLLARCALFVLVAPSCAYQCGPPPLYQLGA 180  
DB 121 SYLPTNTVDALRGSAWGALLRRVGGDVLVHLLARCALFVLVAPSCAYQCGPPPLYQLGA 180  
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DB 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEBATSLEGALSCTRSHSPSVG 300  
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DB 301 RQHHAGPSTSRPPRPWDTPCPVVAETKHFVLSGDKQELRPSFLSSRPSLTGARRL 360  
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DB 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCYPGVLLKTHCPRAAVT 420  
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DB 421 PAAGVCAREKQGSVAAPPEEDTDPRLVQLLRQHSSPWQYVGFVRACLRRLVPPGLWGS 480  
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DB 481 RHNERRFLRNTKKFISLGKHAKLSIQLTWMKSVRDCAWLRSPGVCVPAAEHRLREI 540  
QY 541 LAKFLHMLMSYVVELLRSPFYVTETTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVOLRE 600  
DB 541 LAKFLHMLMSYVVELLRSPFYVTETTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVOLRE 600  
QY 601 LSEAEVQHRREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660  
DB 601 LSEAEVQHRREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660  
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLRVRAODPPPELVFKVDVTGAYDTI 720

Db 661 LFSVLNTERARRPGLLGASVGLDLDIHRAMTTFVLVRQAOPPELVFVKVDVTGAYDTI 720  
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Db 721 PQDLRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPYMQFVAHL 780  
Qy 781 QETSPLRDVAVIEOSSLINEASSGLFDVFLRFMCHHAVIRGKSYVOCQIGIPQGSILSTL 840  
Db 781 QETSPLRDVAVIEOSSLINEASSGLFDVFLRFMCHHAVIRGKSYVOCQIGIPQGSILSTL 840  
Qy 841 LCSLCYGDMEKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900  
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Qy 961 NRGFKAGNRMRKLFVGLRLKCHSLFLDLQVNSIQTVCTNIYKILLQAVRFHACVQLP 1020  
Db 961 NRGFKAGNRMRKLFVGLRLKCHSLFLDLQVNSIQTVCTNIYKILLQAVRFHACVQLP 1020  
Qy 1021 FHOQVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFL 1080  
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Qy 1081 KLTRHRYVYPLGLSLTAQTQLSRKLP GTTLTALAAANPALPSDFKTILD 1132  
Db 1081 KLTRHRYVYPLGLSLTAQTQLSRKLP GTTLTALAAANPALPSDFKTILD 1132

RESULT 3

US-09-843-676-225  
; Sequence 225, Application US/09843676  
; Patent No. US20020164786A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20020164786A1el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/843,676  
; FILING DATE: 26-Apr-2001  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 225:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1132 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 225:  
US-09-843-676-225

Query Match 100.0%; Score 5961; DB 9; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGQWRLVQRGDPAAPRALVAQCLVCVPM 60  
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Db 121 SYLPTNTVDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Qy 181 ATQARPPPHASGPRRLGGERAMNHSVREAGVPLGLPAGARRRGGSASRSLPKRPRR 240  
Db 181 ATQARPPPHASGPRRLGGERAMNHSVREAGVPLGLPAGARRRGGSASRSLPKRPRR 240  
Qy 241 GAAPERTPVGGSWAHPGRTGPGSDRGFCVSPARPABEATSLGALSCTRSHSPSVG 300  
Db 241 GAAPERTPVGGSWAHPGRTGPGSDRGFCVSPARPABEATSLGALSCTRSHSPSVG 300  
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Db 301 RQHAGPPSTSRPPRPMWDTPCPPVYAEKHFLLYSSGDKQLRPSFLLSRPSLTGARRL 360  
Qy 361 VETIFLGSRPWMPGTTPRRLPRLPORYWQMRPLFLELLGNHAQCPIGYVLLKTHCPIRAAT 420  
Db 361 VETIFLGSRPWMPGTTPRRLPRLPORYWQMRPLFLELLGNHAQCPIGYVLLKTHCPIRAAT 420  
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Db 421 PAAGVCAREKPGQSVAAPEBEDTDPRLVOLLRHSSPMQVYGFVRACLRLVPPGLWGS 480  
Qy 481 RHNERRFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGCPVAAEHLREEI 540  
Db 481 RHNERRFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGCPVAAEHLREEI 540  
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Db 541 LAKPLHLMMSVYVVELLRSFFYVTTTFOKNRLLFFYRKSVWSKLQSGIIRHLLKRVQRE 600  
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Db 601 LSEAEVQREARPAALTSRLRFPKPDGLRPIVNM DYVVGARTFREKRAERTLSRVKA 660  
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Db 661 LFSVLNTERARRPGLLGASVGLDLDIHRAMTTFVLVRQAOPPELVFVKVDVTGAYDTI 720  
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Db 721 PQDLRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPYMQFVAHL 780  
Qy 781 QETSPLRDVAVIEOSSLINEASSGLFDVFLRFMCHHAVIRGKSYVOCQIGIPQGSILSTL 840  
Db 781 QETSPLRDVAVIEOSSLINEASSGLFDVFLRFMCHHAVIRGKSYVOCQIGIPQGSILSTL 840

Qy	841	LC	SL	CY	G	D	M	E	N	K	L	F	A	G	I	R	D	G	L	L	R	V	D	D	F	L	L	V	T	P	H	L	T	H	A	K	T	F	L	R	T	L	V	R	G	P	E	Y	G	C	V	N	L	900				
Db	841	LC	SL	CY	G	D	M	E	N	K	L	F	A	G	I	R	D	G	L	L	R	V	D	D	F	L	L	V	T	P	H	L	T	H	A	K	T	F	L	R	T	L	V	R	G	P	E	Y	G	C	V	N	L	900				
Qy	901	R	K	T	V	N	F	P	V	E	D	E	A	L	G	G	T	A	F	V	O	M	P	A	H	G	L	F	P	W	C	G	L	L	D	T	R	T	L	E	V	Q	S	D	S	S	A	R	T	S	I	R	A	S	I	T	F	960
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## RESULT 4

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US-09-953-052-2
; Sequence 2, Application US/09953052
; Patent No. US20020173476A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Antisense Compositions for Detecting and
; Inhibiting Telomerase Reverse Transcriptase
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1 APPLICATION NUMBER: WO PCT/US97/17618
2 FILING DATE: 01-OCT-1997
3 APPLICATION NUMBER: WO PCT/US97/17885
4 FILING DATE: 01-OCT-1997
5 ATTORNEY/AGENT INFORMATION:
6
7 NAME: Parent, Annette S.
8
9 REGISTRATION NUMBER: 42,058
10 REFERENCE/DOCKET NUMBER: 015389-0036000US
11
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: (415) 576-0200
14 TELEFAX: (415) 576-0300
15
16 INFORMATION FOR SEQ ID NO: 2:
17
18 SEQUENCE CHARACTERISTICS:
19
20 LENGTH: 1132 amino acids
21 TYPE: amino acid
22 TOPOLOGY: linear
23
24 MOLECULE TYPE: protein
25
26 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
27
28 US-09-953-052-2

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Query Match	100.0%; Score 5961; DB 9; Length 1132;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1132; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MPRAPRCRAVSLRSHRYEVLPLATFVRRLGPCQWRLVQRGDPAAFRALVAQCLVCVPM 60
Db	
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Db	
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Db	
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Db	
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Qy	181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRPRR 240
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Qy	421 PAAGVCAREKPGQSVAAPEEDTDPRLVLQLRQHSPPWQVYGFVRACLRRLVPPGLWGS 480
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Qy	481 RHNERRFLRNTKXFI SLGKHA KLSLOBLTWKMSVDCNWLRRSPQVGVCPAAEHRLRBEI 540
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Qy	541 LAKFLHLMVSVYVVELLRSPFYFTTTFQKNRLFYFKSVWSKLQSIGIROHLKRVLQRE 600
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Qy	601 LSAEVRQHRHREARPALLTSLRLRPIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
Db	
Qy	601 LSAEVRQHRHREARPALLTSLRLRPIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
Db	
Qy	661 LFSVLNVERARRPGLLGASVLGLDDTHRAWRTFVLVRADPPPELVFKVDVDTGAYDTI 720
Db	
Qy	661 LFSVLNVERARRPGLLGASVLGLDDTHRAWRTFVLVRADPPPELVFKVDVDTGAYDTI 720
Db	
Qy	721 PQDLRTEVIASITKPQNTYCVREYAVVQKAAHGHRKAFKSHSVSTLTDLOPYMROFVAHL 780

[illegible]

## RESULT 5

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US-09-788-110A-23
; Sequence 23, Application US/09788110A
; Publication No. US20040086518A1
; GENERAL INFORMATION:
; APPLICANT: Zanetti, Maurizio
; TITLE OF INVENTION: A Universal Vaccine and Method for Treating Cancer Employing
; TITLE OF INVENTION: Telomerase Reverse Transcriptase
; FILE REFERENCE: UCSD-07017
; CURRENT APPLICATION NUMBER: US/09/788,110A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 1132
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-788-110A-23

```

[illegible]

## RESULT 6

0001 0  
 US-10-053-758-225  
 ; Sequence 225, Application US/10053758  
 ; Publication No. US20030032075A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cech, Thomas R.  
 ; Lingner, Joachim  
 ; Nakamura, Toru  
 ; Chapman, Karen B.  
 ; Morin, Gregg B.  
 ; Harley, Calvin  
 ; Andrews, William H.  
 ; TITLE OF INVENTION: NO. US20030032075A1el Telomerase  
 ; NUMBER OF SEQUENCES: 225  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, 8th Floor  
 ; CITY: San Francisco

/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent In Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/10/053,758  
/ FILING DATE: 18-Jan-2002  
/ CLASSIFICATION: 536  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/854,050  
/ FILING DATE: 09-MAY-1997  
/ APPLICATION NUMBER: US 08/851,843  
/ FILING DATE: 06-MAY-1997  
/ APPLICATION NUMBER: US 08/846,017  
/ FILING DATE: 25-APR-1997  
/ APPLICATION NUMBER: US 08/844,419  
/ FILING DATE: 18-APR-1997  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002930US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 225:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 1132 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 225:  
US-10-053-758-225  
  
Query Match 100.0%; Score 5961; DB 14; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MPAPRCRAVRSLLRSHYREVLPLATEVRLPGQWRLVQRGDPAAPRALVAQCLVCPW 60  
Db 1 MPAPRCRAVRSLLRSHYREVLPLATEVRLPGQWRLVQRGDPAAPRALVAQCLVCPW 60  
  
Qy 61 DARPPAAPSPRQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120  
Db 61 DARPPAAPSPRQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120  
  
Qy 121 SYLPTVTVDALRGSGGALLRRVGGDDVLAHLLARCAFLVLAAPSCAYQVCGPPLVLGA 180  
Db 121 SYLPTVTVDALRGSGGALLRRVGGDDVLAHLLARCAFLVLAAPSCAYQVCGPPLVLGA 180  
  
Qy 181 ATQARPPPHASGPRRRRCERAMNHSVREAGVPLGLPAPGARRRGGSASRLPLPKRPRR 240  
Db 181 ATQARPPPHASGPRRRRCERAMNHSVREAGVPLGLPAPGARRRGGSASRLPLPKRPRR 240  
  
Qy 241 GAPEPRTVPGQSWAHPGTRGSDRGFCVSPAPAEATSLGALSGRTRHSPSVG 300  
Db 241 GAPEPRTVPGQSWAHPGTRGSDRGFCVSPAPAEATSLGALSGRTRHSPSVG 300  
  
Qy 301 ROHHAGPPTSRRPMDTCCPPVATKHFLLYSSGDKQLRPSFLLSLRPSLTGARLL 360  
Db 301 ROHHAGPPTSRRPMDTCCPPVATKHFLLYSSGDKQLRPSFLLSLRPSLTGARLL 360  
  
Qy 361 VETIFLGRSPPMPTGTPRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420  
Db 361 VETIFLGRSPPMPTGTPRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420  
  
Qy 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQVYGVFVRACLRLRLLVPPGLWGS 480

Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQVYGVFVRACLRLRLLVPPGLWGS 480  
Qy 481 RHNERFLNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540  
Db 481 RHNERFLNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540  
Qy 541 LAKFLHLMSSVYVVELLRFFVYVTEFTFQKNRLFYFKRSVWSKLQSIGIRQHLKRVQLRE 600  
Db 541 LAKFLHLMSSVYVVELLRFFVYVTEFTFQKNRLFYFKRSVWSKLQSIGIRQHLKRVQLRE 600  
Qy 601 LSEAEVRQHREARPALLTSRLRPIPKPDGLRPIVNMMDYVVGARTFRREKRAERLTSRVKA 660  
Db 601 LSEAEVRQHREARPALLTSRLRPIPKPDGLRPIVNMMDYVVGARTFRREKRAERLTSRVKA 660  
Qy 661 LFSVLNYERARRPGLLGASVILGDDIHRARWTFVLVRAQDPPPELYFKVDVGTAYDTI 720  
Db 661 LFSVLNYERARRPGLLGASVILGDDIHRARWTFVLVRAQDPPPELYFKVDVGTAYDTI 720  
Qy 721 PDORLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780  
Db 721 PDORLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780  
Qy 781 QETSPLRDADVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOGSI STL 840  
Db 781 QETSPLRDADVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOGSI STL 840  
Qy 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCNVNL 900  
Db 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCNVNL 900  
Qy 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSSVARTSIRASLTF 960  
Db 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSSVARTSIRASLTF 960  
Qy 961 NRGFKAGRNMRRLFGVLRKLCCHSLFLLDQVNSLQVCTNIYKILLQAYRFHACVQLP 1020  
Db 961 NRGFKAGRNMRRLFGVLRKLCCHSLFLLDQVNSLQVCTNIYKILLQAYRFHACVQLP 1020  
Qy 1021 FHQQWKNPTFFLRVISDTASLCYILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080  
Db 1021 FHQQWKNPTFFLRVISDTASLCYILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080  
Qy 1081 KLTRHRVTVPVLLGSLRTAQTOLSRKLPOTTLTALAANAANPALPSDFKTILD 1132  
Db 1081 KLTRHRVTVPVLLGSLRTAQTOLSRKLPOTTLTALAANAANPALPSDFKTILD 1132

RESULT 7

US-10-208-243-2  
; Sequence 2, Application US/10208243  
; Publication No. US20030044394A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaeta, Federico C.A.  
; APPLICANT: Geron Corporation  
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune  
; TITLE OF INVENTION: Response to a Telomerase Antigen  
; FILE REFERENCE: 015389-003500PC  
; CURRENT APPLICATION NUMBER: US/10/208,243  
; CURRENT FILING DATE: 2002-07-30  
; PRIOR APPLICATION NUMBER: US/09/675,321  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/112,006  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898  
; PRIOR FILING DATE: 1999-03-30  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-208-243-2

Query Match	100.0%;	Score 5961;	DB 14;	Length 1132;		
Best Local Similarity	100.0%;	Pred. No. 0;				
Matches 1132;	Conservative	0;	Mismatches	0;	Gaps 0;	
QY	1	MPRAPRCRAVRSLRSHREVLP	PLATFVRR	LGPOGWR	LVQRGDPAAFRALVAQC	LVCPW 60
DB	1	MPRAPRCRAVRSLRSHREVLP	PLATFVRR	LGPOGWR	LVQRGDPAAFRALVAQC	LVCPW 60
QY	61	DARPPAAPSPRQVSC	KLKELVARVLQRLCER	GAKNVLA	FGFALLD	GARGGPEAFTTSVR 120
DB	61	DARPPAAPSPRQVSC	KLKELVARVLQRLCER	GAKNVLA	FGFALLD	GARGGPEAFTTSVR 120
QY	121	SYLPNTVTDALRGSGAWGL	LLLRVGD	VLVHLLAR	CALFVLVAP	SCAYQVCGPPLYQLGA 180
DB	121	SYLPNTVTDALRGSGAWGL	LLLRVGD	VLVHLLAR	CALFVLVAP	SCAYQVCGPPLYQLGA 180
QY	181	ATQARPPHASPGRRLG	CERAWNHSVREAG	VPVLGLPAPGAR	RRGGASAS	RSRLPLPKPRR 240
DB	181	ATQARPPHASPGRRLG	CERAWNHSVREAG	VPVLGLPAPGAR	RRGGASAS	RSRLPLPKPRR 240
QY	241	GAAPERTPVGGWAHPGR	TRGSPDRGFCVSP	PARPAEAT	SLEGALS	GSTRHSPSVG 300
DB	241	GAAPERTPVGGWAHPGR	TRGSPDRGFCVSP	PARPAEAT	SLEGALS	GSTRHSPSVG 300
QY	301	ROHAGPPTSPRPP	PDWTPCPVVAET	KHFYSSG	DEQELRPS	FLSSLRPSLTGARRL 360
DB	301	ROHAGPPTSPRPP	PDWTPCPVVAET	KHFYSSG	DEQELRPS	FLSSLRPSLTGARRL 360
QY	361	VETIFLGSPPWPGT	PRRLPRLPOR	YOMWRPLFLELLGN	HAOCYGVLLK	THCPLRAAVT 420
DB	361	VETIFLGSPPWPGT	PRRLPRLPOR	YOMWRPLFLELLGN	HAOCYGVLLK	THCPLRAAVT 420
QY	421	PAAGVCAREKPOGS	VAAPEEEDTPRR	LVQLLRQHS	SPWQYGFVRA	CLRLRVPPLGWS 480
DB	421	PAAGVCAREKPOGS	VAAPEEEDTPRR	LVQLLRQHS	SPWQYGFVRA	CLRLRVPPLGWS 480
QY	481	RNNRRFLNTK	TKFISLGKHAKLS	LOELTKWMS	VRDCAWLRRSPGV	CVPAAEHRLREEI 540
DB	481	RNNRRFLNTK	TKFISLGKHAKLS	LOELTKWMS	VRDCAWLRRSPGV	CVPAAEHRLREEI 540
QY	541	LAKFLHMLSVV	VVELLSRFFVVT	TETQKNR	LFFYRKS	VMSKLSIGIROHLKRVOLRE 600
DB	541	LAKFLHMLSVV	VVELLSRFFVVT	TETQKNR	LFFYRKS	VMSKLSIGIROHLKRVOLRE 600
QY	601	LSEAEVQREHREAR	PALLTSRLRFI	PKDGLRPI	VNMDDVVGART	FRREKRAERLTSRVKA 660
DB	601	LSEAEVQREHREAR	PALLTSRLRFI	PKDGLRPI	VNMDDVVGART	FRREKRAERLTSRVKA 660
QY	661	LFSVLNYERARR	PGLLGASVLG	LDIHRART	FVLVR	QAQDPPPELYFVKVDVTGAYDTI 720
DB	661	LFSVLNYERARR	PGLLGASVLG	LDIHRART	FVLVR	QAQDPPPELYFVKVDVTGAYDTI 720
QY	721	PODRLTEVI	ASIIKQNTYCV	RRYAVVQKA	AGHVVRKAFK	SHVSTLTDLOQYMQFVAHL 780
DB	721	PODRLTEVI	ASIIKQNTYCV	RRYAVVQKA	AGHVVRKAFK	SHVSTLTDLOQYMQFVAHL 780
QY	781	QETSPURDAV	LEQSSLINEAS	SGLFDVFLR	PMCHAVRIR	KSVMCOQIPQGSILSTL 840
DB	781	QETSPURDAV	LEQSSLINEAS	SGLFDVFLR	PMCHAVRIR	KSVMCOQIPQGSILSTL 840
QY	841	LCSLCYGD	MENKLFAGIR	DGGLLRV	DDFLVTPH	LTHAKTFLRTLVRGVPYGCVVNL 900
DB	841	LCSLCYGD	MENKLFAGIR	DGGLLRV	DDFLVTPH	LTHAKTFLRTLVRGVPYGCVVNL 900
QY	901	RKTVMN	FPVEDEALGT	AFVQMP	AGLFPWC	GLLTDLTLEVSQDYSYARTSTRASLTIF 960
DB	901	RKTVMN	FPVEDEALGT	AFVQMP	AGLFPWC	GLLTDLTLEVSQDYSYARTSTRASLTIF 960
QY	961	NRGFKAGR	NMRKLFVLR	FLKCHSLF	LDLQVNS	LOTCTNLYKILLQAVFHCVLQLP 1020
DB	961	NRGFKAGR	NMRKLFVLR	FLKCHSLF	LDLQVNS	LOTCTNLYKILLQAVFHCVLQLP 1020
QY	1021	FHQQVWKNP	TFFLRVIS	DTASLCYS	ITLAKAKNAG	MSLGAKGAGPLPSEAVQWLCHQAFLL 1080

Db 61 DARPPAAPSPFQVSCUKELVARVLQRLCERGAKNVLAFGFALLDGGARGPPEAFTTSVR 120  
Qy 121 SYLPTNTVDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Db 121 SYLPTNTVDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Qy 181 ATQARPPPHASGPRRRRLGGERAMNHSVREAGVPLGLPAPGARRGGGSASRSLPLPKRPRR 240  
Db 181 ATQARPPPHASGPRRRRLGGERAMNHSVREAGVPLGLPAPGARRGGGSASRSLPLPKRPRR 240  
Qy 241 GAAPPEPTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSGTRHSHPSVG 300  
Db 241 GAAPPEPTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSGTRHSHPSVG 300  
Qy 301 ROHAGAPPSRPPRPMDTCPVYAEKHFLLXSSGDKQOLRPSFLLSLSLRPSLTGARRL 360  
Db 301 ROHAGAPPSRPPRPMDTCPVYAEKHFLLXSSGDKQOLRPSFLLSLSLRPSLTGARRL 360  
Qy 361 VETIFLGSRRPMPGTPRRRLPRLPQRYWQMRPLFELILGNHAQCPYGVLLKTHCPLRAAVT 420  
Db 361 VETIFLGSRRPMPGTPRRRLPRLPQRYWQMRPLFELILGNHAQCPYGVLLKTHCPLRAAVT 420  
Qy 421 PAAGVCAREKPGQSVAAPEBEDTDPRLVOLLRQHSSFPWQYGFVRACLRLVPPGLWGS 480  
Db 421 PAAGVCAREKPGQSVAAPEBEDTDPRLVOLLRQHSSFPWQYGFVRACLRLVPPGLWGS 480  
Qy 481 RHNERRLNTKPFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540  
Db 481 RHNERRLNTKPFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540  
Qy 541 LAKFLHLMSSVYVVELLSRFFYVTTETTFQKNRFFFYKRSYWSKLQSIGIRQHLKRVQLE 600  
Db 541 LAKFLHLMSSVYVVELLSRFFYVTTETTFQKNRFFFYKRSYWSKLQSIGIRQHLKRVQLE 600  
Qy 601 LSEAEVQREARPALITSRLFTPKDGLRPIVNMDDYVVGARTFRREKGAERLTSRVKA 660  
Db 601 LSEAEVQREARPALITSRLFTPKDGLRPIVNMDDYVVGARTFRREKGAERLTSRVKA 660  
Qy 661 LFSVLNVERARRPGLGASVLGDDIHRWRTFVLRVRAODPPPELYFVKVDVTGAYDTI 720  
Db 661 LFSVLNVERARRPGLGASVLGDDIHRWRTFVLRVRAODPPPELYFVKVDVTGAYDTI 720  
Qy 721 PQDLRLTEVIAIIKPNQTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPYMRQFVAHL 780  
Db 721 PQDLRLTEVIAIIKPNQTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPYMRQFVAHL 780  
Qy 781 QETSPLRDADVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOGSIILSTL 840  
Db 781 QETSPLRDADVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOGSIILSTL 840  
Qy 841 LCSLCYGD MENKLPAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGPVPGCVNVL 900  
Db 841 LCSLCYGD MENKLPAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGPVPGCVNVL 900  
Qy 901 RKTWNPNVDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVDSDYSYSSVARTSIRASLTF 960  
Db 901 RKTWNPNVDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVDSDYSYSSVARTSIRASLTF 960  
Qy 961 NRGFKAGNRNRKLFVGLRLKCHSLFLDLQVNSLQVCTNIIYKILLQAVRFHACVQLQP 1020  
Db 961 NRGFKAGNRNRKLFVGLRLKCHSLFLDLQVNSLQVCTNIIYKILLQAVRFHACVQLQP 1020  
Qy 1021 FHOQVKNPPTFFLRVSDTASLCVSIILKAKNAGSLGAKGAAGPLPSEAVQWILCHQAFLL 1080  
Db 1021 FHOQVKNPPTFFLRVSDTASLCVSIILKAKNAGSLGAKGAAGPLPSEAVQWILCHQAFLL 1080  
Qy 1081 KLTRHRVTVYVPLLGSLRTAQTLRSRKLPGTTLTALFAAANPALPSPFKTILD 1132  
Db 1081 KLTRHRVTVYVPLLGSLRTAQTLRSRKLPGTTLTALFAAANPALPSPFKTILD 1132

RESULT 9

US-10-054-611-225

; Sequence 225, Application US/10054611  
; Publication No. US20030059787A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20030059787A1el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/054,611  
; FILING DATE: 18-Jan-2002  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/854,050  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 225:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1132 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 225:  
US-10-054-611-225

Query Match 100.0%; Score 5961; DB 14; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRAFCRAVRSLRSHREVLPATFVRRLLPQGWRLVQRGDPAAAFRALVAQCLVCVPW 60  
Db 1 MPRAFCRAVRSLRSHREVLPATFVRRLLPQGWRLVQRGDPAAAFRALVAQCLVCVPW 60  
Qy 61 DARPPAAPSPFQVSCUKELVARVLQRLCERGAKNVLAFGFALLDGGARGPPEAFTTSVR 120  
Db 61 DARPPAAPSPFQVSCUKELVARVLQRLCERGAKNVLAFGFALLDGGARGPPEAFTTSVR 120  
Qy 121 SYLPTNTVDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Db 121 SYLPTNTVDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Qy 181 ATQARPPPHASGPRRRRLGGERAMNHSVREAGVPLGLPAPGARRGGGSASRSLPLPKRPRR 240  
Db 181 ATQARPPPHASGPRRRRLGGERAMNHSVREAGVPLGLPAPGARRGGGSASRSLPLPKRPRR 240



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Qy 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEBEATSLEGALSCTRHSHPVG 300
Db 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEBEATSLEGALSCTRHSHPVG 300
Qy 301 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQELRPFLLSSLRPSLTGARRL 360
Db 301 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQELRPFLLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSPPWQYGVFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSPPWQYGVFVRACLRRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKKFISLGKHAHKLISLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERRFLRNTKKFISLGKHAHKLISLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
Qy 541 LAKFLHMLMSVYVVELLRSFFYVTTTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVQJRE 600
Db 541 LAKFLHMLMSVYVVELLRSFFYVTTTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVQJRE 600
Qy 601 LSEAEVQREARPAALITSRLRFPDKDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVQREARPAALITSRLRFPDKDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNVERARRPGLGASVLGLDDIHRWRTFVLVRADQPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLGASVLGLDDIHRWRTFVLVRADQPPPELYFVKVDVTGAYDTI 720
Qy 721 QDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780
Db 721 QDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780
Qy 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOQSILSTL 840
Db 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOQSILSTL 840
Qy 841 LCSICYGDMENKLFAGTRDGLLRVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Db 841 LCSICYGDMENKLFAGTRDGLLRVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Qy 901 RKTVVNFVEDEALGCTAFVQMPAHGLFPWCGLLDDRTLEVDQSDYSYARTSRASLTIF 960
Db 901 RKTVVNFVEDEALGCTAFVQMPAHGLFPWCGLLDDRTLEVDQSDYSYARTSRASLTIF 960
Qy 961 NRGFKAGNMRRKLFVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNMRRKLFVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Qy 1021 PHQOVKNPTFFLAVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 PHQOVKNPTFFLAVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLGLSLRTAQQLSRKLP GTTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGLSLRTAQQLSRKLP GTTTLTALEAAANPALPSDFKTILD 1132
RESULT 10
US-10-105-963-2
; Sequence 2, Application US/10105963
; Publication No. US200300688181
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Denning, Chris
; APPLICANT: Clark, A. John
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: Animal tissue with Carbohydrate Antigens Compatible for Human
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
; TITLE OF INVENTION: Recombination
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; FILE REFERENCE: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-105-963-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRSLLRSHYREVLPATFVRLRPGQHRLVQGDPAAPRALVAOCLVCVPW 60
Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRLRPGQHRLVQGDPAAPRALVAOCLVCVPW 60
Qy 61 DARPPPAAPSFROVSCIKELVARVLQRLCERGAKNVLAFGFALLDGGARGGPPPAFTTSVR 120
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Db 121 SYLPTNTVDALRGSGAWGALLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATOARPPPHASGPRRLGCERANHSVREAGVPLGLPAGARRRGSGASRLPLPKPRR 240
Db 181 ATOARPPPHASGPRRLGCERANHSVREAGVPLGLPAGARRRGSGASRLPLPKPRR 240
Qy 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEBEATSLEGALSCTRHSHPVG 300
Db 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEBEATSLEGALSCTRHSHPVG 300
Qy 301 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQELRPSFLLSSLRPSLTGARRL 360
Db 301 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQELRPSFLLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSPPWQYGVFVRACLRRLVPPGLWGS 480
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Db 481 RHNERRFLRNTKKFISLGKHAHKLISLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
Qy 541 LAKFLHMLMSVYVVELLRSFFYVTTTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVQJRE 600
Db 541 LAKFLHMLMSVYVVELLRSFFYVTTTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVQJRE 600
Qy 601 LSEAEVQREARPAALITSRLRFPDKDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVQREARPAALITSRLRFPDKDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNVERARRPGLGASVLGLDDIHRWRTFVLVRADQPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLGASVLGLDDIHRWRTFVLVRADQPPPELYFVKVDVTGAYDTI 720
Qy 721 QDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780
Db 721 QDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780
Qy 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOQSILSTL 840
Db 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOQSILSTL 840
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QY 841 LCSLCYGMENKLFAGIRRDGILLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900  
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QY 901 RKTVMNFFVEDEALGGTAFVQMPAHGLFPWCGLLDLRTLLEVQSDYSYARTSIRASLTFF 960  
Db 901 RKTVMNFFVEDEALGGTAFVQMPAHGLFPWCGLLDLRTLLEVQSDYSYARTSIRASLTFF 960  
QY 961 NRGFKAGNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020  
Db 961 NRGFKAGNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020  
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Db 1021 FHQQWKNPFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080  
QY 1081 KLTHRVITYVPLLSGLRTAQQLSRKLPFGTTLTLEAANPALPSPDKTILD 1132  
Db 1081 KLTHRVITYVPLLSGLRTAQQLSRKLPFGTTLTLEAANPALPSPDKTILD 1132  
RESULT 11  
US-10-044-692-2  
; Sequence 2, Application US/10044692  
; Publication No. US20030096344A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
; THERAPEUTIC METHODS  
; NUMBER OF SEQUENCES: 335  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/044,692  
; FILING DATE: 11-Jan-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/912,951  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002600US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1132 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-044-692-2  
Query Match 100.0%; Score 5961; DB 14; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPRAPRCRAVRSLLRSHREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60  
Db 1 MPRAPRCRAVRSLLRSHREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60  
QY 61 DARPPPAAPSFQVSCLEKELVARVQLQRCERGAKNVLAFGFALLDCARGGPPAEFTTSVR 120  
Db 61 DARPPPAAPSFQVSCLEKELVARVQLQRCERGAKNVLAFGFALLDCARGGPPAEFTTSVR 120  
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Db 121 SYLPNTVTDALRGSGAWGLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLVOLGA 180  
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Db 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGASRSPLPKRPRR 240  
QY 241 GAAPEPERTVQGGSWAHGPRTRGSDRGFCVVSPPARPAEAEATSLGALSGTRHSHPSVG 300  
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QY 421 PAAGVCAREKPOGSAVAPEEEDTPRRLLVOLLRQHSHPQVYGFVRACLRRLRVLPPGLWGS 480  
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QY 481 RHNERPFLNKKFISLGHAKLSQELTWKMSVRDCAWLRRSPGVCGVPAAEHRLREI 540  
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QY 601 LSEAEVRQHRARPALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKAEERLTSRVKA 660  
Db 601 LSEAEVRQHRARPALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKAEERLTSRVKA 660  
QY 661 LFSVLNVERARPPGLLGASVLGLDIIHRAWRTFVLRAQDPPPELYFKVDVTGAYDTI 720  
Db 661 LFSVLNVERARPPGLLGASVLGLDIIHRAWRTFVLRAQDPPPELYFKVDVTGAYDTI 720  
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QY 841 LCSLCYGMENKLFAGIRRDGILLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900  
Db 841 LCSLCYGMENKLFAGIRRDGILLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900  
QY 901 RKTVMNFFVEDEALGGTAFVQMPAHGLFPWCGLLDLRTLLEVQSDYSYARTSIRASLTFF 960

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Qy 961 NRGFKAGNMRRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020  
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RESULT 12

US-10-044-539-2  
; Sequence 2, Application US/10044539  
; Publication No. US2003010093A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
; THERAPEUTIC METHODS  
; NUMBER OF SEQUENCES: 335  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/044,539  
; FILING DATE: 11-Jan-2002  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/912,951  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 19-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-0026000US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1132 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-044-539-2  
Query Match 100.0%; Score 5961; DB 14; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRAPRCRAVRSLLRSHYREYVLPATFVRLRPGQWRLVORGDPAAFRALVAQCLVCVPW 60  
Db 1 MPRAPRCRAVRSLLRSHYREYVLPATFVRLRPGQWRLVORGDPAAFRALVAQCLVCVPW 60  
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Db 61 DARPPPAAPRQVSCIKELVARVLQRLCERGAKNVLAFGPALLDGDARGGPPPEAFTTSVR 120  
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Qy 421 PAAGVCAREKPGQSVAAPEBEDTDPRLVQLLRQHSPPWQYGFVRACLRLRVLPPGLMGS 480  
Db 421 PAAGVCAREKPGQSVAAPEBEDTDPRLVQLLRQHSPPWQYGFVRACLRLRVLPPGLMGS 480  
Qy 481 RHNERRFLRNTKFPISLGKHAJLSQELTWKMSVRDCAWLRSPGVCGVPAAEHRLREI 540  
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Qy 841 LCSLCYGD MENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLTRVGVPEYGCVVNL 900  
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RESULT 13

US-10-295-681-57

; Sequence 57, Application US/10295681

; Publication No. US20030166270A1

GENERAL INFORMATION:

APPLICANT: E. Premkumar Reddy

APPLICANT: Sushil G. Rane

APPLICANT: Richard V. Mettus

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REVERSIBLY

TITLE OF INVENTION: INDUCING CONTINUAL GROWTH IN NORMAL CELLS

FILE REFERENCE: 6056-307

CURRENT APPLICATION NUMBER: US/10/295.681

CURRENT FILING DATE: 2002-11-15

PRIOR APPLICATION NUMBER: US 60/334,760

PRIOR FILING DATE: 2001-11-15

NUMBER OF SEQ ID NOS: 69

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 57

LENGTH: 1132

TYPE: PRT

ORGANISM: Homo sapiens

US-10-295-681-57

Query Match 100.0%; Score 5961; DB 14; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPCRVRSLLRSHYREVLPATFVRRLGPGWRLVQGDPPAARFALVACQVCVPV 60

Db 1 MPRAPCRVRSLLRSHYREVLPATFVRRLGPGWRLVQGDPPAARFALVACQVCVPV 60

Qy 61 DARPPAAPSPROVSCLEKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

Db 61 DARPPAAPSPROVSCLEKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

Qy 121 SYLNTVTDALRGSGALLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db 121 SYLNTVTDALRGSGALLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy 181 ATQARPPHAGPERRRIGCERAMNHSVREAGVPLGLPAGARRGGSSASRLPLPKPRR 240

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Db 481 RHNERRLNTKKFISLGKHAJLSQBLTWKMSVRDCAWLRRSPGVCGVPAASHRLREEI 540

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Db 541 LAKFLHMLSVYVVELLRSEFFVYTTETTFQKNRUFFFYRKSVWSKLSQIGIRQHILKRVOLRE 600

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Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRPFVLVRAQDPPPELYFVKVDVTGAYDTI 720

Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRPFVLVRAQDPPPELYFVKVDVTGAYDTI 720

Qy 721 PQDRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780

Db 721 PQDRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780

Qy 781 QETSPLRDVAVIEQSSSLNEASSGLDFVLRPMCHHAVIRGKSYVQCQIPQGSILSTL 840

Db 781 QETSPLRDVAVIEQSSSLNEASSGLDFVLRPMCHHAVIRGKSYVQCQIPQGSILSTL 840

Qy 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCYNL 900

Db 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCYNL 900

Qy 901 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVQSDYSSVARTSIRASLTF 960

Db 901 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVQSDYSSVARTSIRASLTF 960

Qy 961 NRGFAGNRMRKLVGLRKLCHSLDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020

Db 961 NRGFAGNRMRKLVGLRKLCHSLDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020

Qy 1021 FHQVWKNPTFELRVISDASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080

Db 1021 FHQVWKNPTFELRVISDASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080

Qy 1081 KLTHRVTVYVLLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTLTD 1132

Db 1081 KLTHRVTVYVLLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTLTD 1132

RESULT 14

US-10-325-810-2

; Sequence 2, Application US/10325810

; Publication No. US20030204069A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin B.

APPLICANT: Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/10/325,810

APPLICATION NUMBER: US/10/325,810

FILING DATE: 20-Dec-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181  
FILING DATE: 29-Sep-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1132 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-325-810-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLPGQWRLVQRGDPAARALVAQCLVCVPW 60  
DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLPGQWRLVQRGDPAARALVAQCLVCVPW 60  
QY 61 DARPPAAPSPROVSCLELVARVLQRLCERGANVLAFAFGALDARGGPPPEAFTTSVR 120  
DB 61 DARPPAAPSPROVSCLELVARVLQRLCERGANVLAFAFGALDARGGPPPEAFTTSVR 120  
QY 121 SYLPTVTDALRGSGANGLLLRRVGDVVLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
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QY 181 ATQARPPHAGSPRRRLGCRANWHSVREAGVPLGLPAGNRRGGSGASRLPLPKPRR 240  
DB 181 ATQARPPHAGSPRRRLGCRANWHSVREAGVPLGLPAGNRRGGSGASRLPLPKPRR 240  
QY 241 GAAPEPRTPVQGSWAHPGRTGSPDRGFCVSPARPABEATSLGALSGTRHSHPSVG 300  
DB 241 GAAPEPRTPVQGSWAHPGRTGSPDRGFCVSPARPABEATSLGALSGTRHSHPSVG 300  
QY 301 RQHAGPPSTSRPPMDTPCPVYAEYKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360  
DB 301 RQHAGPPSTSRPPMDTPCPVYAEYKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360  
QY 361 VETIFLGSRPMPGTPRRLLPRLPORYQWQMRPLFLELLGNHAQCYPGYVLLKTHCPRAAVT 420  
DB 361 VETIFLGSRPMPGTPRRLLPRLPORYQWQMRPLFLELLGNHAQCYPGYVLLKTHCPRAAVT 420  
QY 421 PAAGVCAREKPGQSVAAPEEDTPRLVQLLRHSSPQWYGVFVRACLRLVPPGLWGS 480  
DB 421 PAAGVCAREKPGQSVAAPEEDTPRLVQLLRHSSPQWYGVFVRACLRLVPPGLWGS 480  
QY 481 RHNERRFLRNTKKFISLGKHAKLSQELTWKMSVRDCAWLRRSPGVGCPVAAEHLREEL 540

DB 481 RHNERRFLRNTKKFISLGKHAKLSQELTWKMSVRDCAWLRRSPGVGCPVAAEHLREEL 540  
QY 541 LAKFLHLMVSVYVVELLSRFFYVTEFTFOKNRFFFYKSKVMSKLSQSIGIQHLKRVOLRE 600  
DB 541 LAKFLHLMVSVYVVELLSRFFYVTEFTFOKNRFFFYKSKVMSKLSQSIGIQHLKRVOLRE 600  
QY 601 LSAEVRQHREARPAALLTSRLRPIPKPDGLRPIVNMDDYVVGARTFRREKKAERLTSRVKA 660  
DB 601 LSAEVRQHREARPAALLTSRLRPIPKPDGLRPIVNMDDYVVGARTFRREKKAERLTSRVKA 660  
QY 661 LPSVLNYERARRRGLLGASVLGLDDITHRAWRTFVLVRADDPPELYFVKVDVTGAYDTI 720  
DB 661 LPSVLNYERARRRGLLGASVLGLDDITHRAWRTFVLVRADDPPELYFVKVDVTGAYDTI 720  
QY 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780  
DB 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780  
QY 781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPOGSIILSTL 840  
DB 781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPOGSIILSTL 840  
QY 841 LCSLCYGD MENKLFAGIRRDGILLRLVDDDELLVTPHLTHAKTFLRTLVRGVPEYGCYVNL 900  
DB 841 LCSLCYGD MENKLFAGIRRDGILLRLVDDDELLVTPHLTHAKTFLRTLVRGVPEYGCYVNL 900  
QY 901 RKTWNPFVEDEALGGTAFVQMPAHGLFPMCGLLLDLTRLTLEVDSDSYARTSIRASLTF 960  
DB 901 RKTWNPFVEDEALGGTAFVQMPAHGLFPMCGLLLDLTRLTLEVDSDSYARTSIRASLTF 960  
QY 961 NRGFKAGRNMRRLFGVLRLLKCHSLFDLDQVNSLQVTCTNIYKILLQAYRFHACVLQLP 1020  
DB 961 NRGFKAGRNMRRLFGVLRLLKCHSLFDLDQVNSLQVTCTNIYKILLQAYRFHACVLQLP 1020  
QY 1021 FHOQWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080  
DB 1021 FHOQWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080  
QY 1081 KLTRHRVTVYVPLLSGLRTAQTQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132  
DB 1081 KLTRHRVTVYVPLLSGLRTAQTQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132

RESULT 15  
US-10-388-578-2  
; Sequence 2, Application US/10388578  
; Publication No. US2003022441A1  
; GENERAL INFORMATION:  
; APPLICANT: Stanton, Lawrence  
; APPLICANT: Geron Corporation  
; APPLICANT: Ralph, Brandenberger  
; APPLICANT: Joseph, Gold D.  
; APPLICANT: John, Irving  
; APPLICANT: Mandalam, Ramkumar  
; APPLICANT: Mok, Michael  
; APPLICANT: Shelton, Dawne  
; TITLE OF INVENTION: Genes that are Up- or Down-Regulated During Differentiation of H  
; TITLE OF INVENTION: Embryonic Stem Cells  
; FILE REFERENCE: 135/001  
; CURRENT APPLICATION NUMBER: US/10/388,578  
; CURRENT FILING DATE: 2003-03-13  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: Custom  
; SEQ ID NO 2  
; LENGTH: 1132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-388-578-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPOGWRVLVQRGDPAAPRALVAOCLVCVPW	60
Db	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPOGWRVLVQRGDPAAPRALVAOCLVCVPW	60
QY	61	DARPPAAPSPRQVSCLELVARVLQRLCERGAKNVLAFGPFALLDARGGPEAFTTSVR	120
Db	61	DARPPAAPSPRQVSCLELVARVLQRLCERGAKNVLAFGPFALLDARGGPEAFTTSVR	120
QY	121	SYLPNTVTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPELYQLGA	180
Db	121	SYLPNTVTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPELYQLGA	180
QY	181	ATOARPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRRGGASRSLLPLPKRPRR	240
Db	181	ATOARPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRRGGASRSLLPLPKRPRR	240
QY	241	GAAPPERTPVQGSWAHPGTRGFSDRGFCVVSAPARPAEBEATSLEGALSGTRHSHPSVG	300
Db	241	GAAPPERTPVQGSWAHPGTRGFSDRGFCVVSAPARPAEBEATSLEGALSGTRHSHPSVG	300
QY	301	ROHAGPEPSTSRPPRPWDTPCPVYAEKHFYSSGDKQOLRPSFLLSSLRPSLTGARRL	360
Db	301	ROHAGPEPSTSRPPRPWDTPCPVYAEKHFYSSGDKQOLRPSFLLSSLRPSLTGARRL	360
QY	361	VETIFLGSRPWPMPGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT	420
Db	361	VETIFLGSRPWPMPGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT	420
QY	421	PAAGVCAREKPGQSVAAPEEBDDTPRRLVQLLRHSSPQWQYGFVRACLRRLVPPGLWGS	480
Db	421	PAAGVCAREKPGQSVAAPEEBDDTPRRLVQLLRHSSPQWQYGFVRACLRRLVPPGLWGS	480
QY	481	RHNERRRFLRNTKFIISLGKAKLSLOELTWKMSVRDCAWLRBSPGVCVPAAEHRLREEI	540
Db	481	RHNERRRFLRNTKFIISLGKAKLSLOELTWKMSVRDCAWLRBSPGVCVPAAEHRLREEI	540
QY	541	LAKFLHMLMSYVVVELLSRFFYVTETTFQKNRFFFYRKSVMKSQSIGIRQHLKRVQLRE	600
Db	541	LAKFLHMLMSYVVVELLSRFFYVTETTFQKNRFFFYRKSVMKSQSIGIRQHLKRVQLRE	600
QY	601	LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFRREKKAERLTSRVKA	660
Db	601	LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFRREKKAERLTSRVKA	660
QY	661	LFSVLNVERARRPGLLGASVLGLDDIHRAWRTFVLVRADPPPELYFVKVDVTGAYDTI	720
Db	661	LFSVLNVERARRPGLLGASVLGLDDIHRAWRTFVLVRADPPPELYFVKVDVTGAYDTI	720
QY	721	PQDRLTEVIAIIKPNQTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL	780
Db	721	PQDRLTEVIAIIKPNQTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL	780
QY	781	QETSPLRDADVIEQSSSLNEASSGLFDVFLRPMCHHAVIRIGKSYVQCQIPOGSSILSTL	840
Db	781	QETSPLRDADVIEQSSSLNEASSGLFDVFLRPMCHHAVIRIGKSYVQCQIPOGSSILSTL	840
QY	841	LCSLCYGDMENTKLFAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL	900
Db	841	LCSLCYGDMENTKLFAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL	900
QY	901	RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVQSDYSSYARTSIRASLTF	960
Db	901	RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVQSDYSSYARTSIRASLTF	960
QY	961	NRGFKAGRNMRKLFVGLRLKCHSLFLDLQVNSLQVCTNIYKILLQAYRFHACVQLQP	1020
Db	961	NRGFKAGRNMRKLFVGLRLKCHSLFLDLQVNSLQVCTNIYKILLQAYRFHACVQLQP	1020
QY	1021	FHQQVWKNPTFFFLRVISDTSASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL	1080
Db	1021	FHQQVWKNPTFFFLRVISDTSASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL	1080

QY	1081	KLTRHRVTYVPLLGSLRTAQOLSRKLPSTTLTALEAAANPALPSDFKTILD	1132
Db	1081	KLTRHRVTYVPLLGSLRTAQOLSRKLPSTTLTALEAAANPALPSDFKTILD	1132

Search completed: January 10, 2005, 17:51:30  
Job time : 171 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 10, 2005, 17:23:35 ; Search time 50 Seconds  
(without alignments)  
2178.348 Million cell updates/sec

Title: US-10-053-758-225  
Perfect score: 5961  
Sequence: 1 MPRAPRCRAVRSLLRSHYRE.....TALEAAANPALPSDFKTILD 1132  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79.\*  
1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	1132	T03844	telomerase catalyt
2	724.5	12.2	1123	T51517	telomerase reverse
3	594.5	10.0	989	T03838	telomerase catalyt
4	395	6.6	1132	T31107	telomerase reverse
5	363	6.1	1117	T14891	telomerase (EC 2.7
6	356.5	6.0	884	S53396	telomerase catalyt
7	176.5	3.0	3530	A59266	unconventional myo
8	172.5	2.9	660	Q0BE3	BHLF1 protein - hu
9	144	2.4	3511	A59295	unconventional myo
10	142.5	2.4	1560	T00080	hypothetical prote
11	140.5	2.4	1892	T18314	hypothetical prote
12	140	2.3	1460	1 EDBE1F	immediate-early pr
13	139.5	2.3	552	T75311	ABC transporter, A
14	138.5	2.3	924	S27923	gene LF3 protein -
15	135	2.3	1356	1 C45219	N-methyl-D-asparta
16	134.5	2.3	946	T07810	inositol 1,4,5-tri
17	134	2.2	606	TJ3502	orotidine 5'-phosp
18	133	2.2	1106	TJ0405	hypothetical 119.5
19	132	2.2	860	S55543	RNA-directed DNA p
20	131.5	2.2	1184	TG01763	atrophin-1 - human
21	131	2.2	1446	1 A45344	immediate-early pr
22	130.5	2.2	1184	TJ3049	atrophin-1 - human
23	130.5	2.2	2715	T21309	eyelid - fruit fly
24	129.5	2.2	383	S32975	gene BCRF2 protein
25	129	2.2	403	TJ3296	prpL2 protein - hu
26	129	2.2	1776	TG86280	protein T5E21.13 [
27	128.5	2.2	628	TJ01955	hypothetical prote
28	128	2.1	376	TJ75580	adenine deaminase-
29	127.5	2.1	1048	TJ31425	C-terminal domain-

ALIGNMENTS

RESULT 1

T03844  
telomerase catalytic chain - human  
N:Alternate names: telomerase reverse transcriptase  
C:Species: Homo sapiens (man)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T03844  
P:Kakumura, T.M.; Marin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.  
Science 277, 955-959, 1997  
A:Title: telomerase catalytic subunit homologs from fission yeast and human.  
A:Reference number: Z15111; MUID:97400623; PMID:9252327  
A:Accession: T03844  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1132 <NAK>  
A:Cross-references: UNIPROT:O14746; EMBL:AF015950; NID:g2330016; PIDN:AAC51672.1; PID:g  
A:Experimental source: kidney  
C:Genetics:  
A:Gene: TRT  
A:Map position: 5p

Query Match	100.0%;	Score	5961;	DB	2;	Length	1132;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	1132;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLGPGQWRLVORGDPAAFRALVAQCLVCVPW	60			
Db	1	MPRAPRCRAVRSLLRSHYREVLP	PLATEFVRRLGPGQWRLVORGDPAAFRALVAQCLVCVPW	60			
Qy	61	DARPPPAAPSFROVSCLELVARVLQRLCERGA	KNVLAFGFALLDGGARGGPEAFTTSVR	120			
Db	61	DARPPPAAPSFROVSCLELVARVLQRLCERGA	KNVLAFGFALLDGGARGGPEAFTTSVR	120			
Qy	121	SYLPNTVTDALRGSGAWGLLRRVGGDVLVHLLAR	CALFVLVAPSCAYVCGPPLYQLGA	180			
Db	121	SYLPNTVTDALRGSGAWGLLRRVGGDVLVHLLAR	CALFVLVAPSCAYVCGPPLYQLGA	180			
Qy	181	ATOARPPPHASGRRRLGCRANHSVREAGVPLGLP	AGARRRGGSASRLPLPKPRR	240			
Db	181	ATOARPPPHASGRRRLGCRANHSVREAGVPLGLP	AGARRRGGSASRLPLPKPRR	240			
Qy	241	GAAPERTPVGGGSMHAGRTGPSDRGFCVVS	PARPAEATSEALSGTRSHSVSG	300			
Db	241	GAAPERTPVGGGSMHAGRTGPSDRGFCVVS	PARPAEATSEALSGTRSHSVSG	300			
Qy	301	QOHAGPPSTSRPRPMDTCCPPVYATKHFLYSSG	DKQLRPSFLSSLRPSLTGARRL	360			
Db	301	QOHAGPPSTSRPRPMDTCCPPVYATKHFLYSSG	DKQLRPSFLSSLRPSLTGARRL	360			
Qy	361	VETIFLGSRPWMPGTPRRLPRLPORYWQMRPLF	LELLGNHAQCYPYGVLLKTHCPLRAVT	420			
Db	361	VETIFLGSRPWMPGTPRRLPRLPORYWQMRPLF	LELLGNHAQCYPYGVLLKTHCPLRAVT	420			

proline-rich prote  
actin-depolymexizi  
probable mucin DKF  
mixed-lineage prot  
hypothetical prote  
hypothetical prote  
probable nucleic a  
transposase, uncha  
pol protein - silk  
Wiskott-Aldrich sy  
viral proteinase -  
tenascin Y precurs  
immediate-early pr  
N-methyl-D-asparta  
hypothetical prote

```
QY 421 PAAGVCAREKPGSVAAPBEEDTDRRLVQLLRQSHSPMOVYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGSVAAPBEEDTDRRLVQLLRQSHSPMOVYGFVRACLRRLVPPGLWGS 480
QY 481 RNERRPLNTKFTSLGKHAKLSLOELTWKMSVDCAWLRSPGVGCPAAEHLREEI 540
Db 481 RNERRPLNTKFTSLGKHAKLSLOELTWKMSVDCAWLRSPGVGCPAAEHLREEI 540
QY 541 LAKFLHLMMSVVVVELLSFFVTETTFQKRLFFYRKSVWSKQSIGIROHLKRVQLE 600
Db 541 LAKFLHLMMSVVVVELLSFFVTETTFQKRLFFYRKSVWSKQSIGIROHLKRVQLE 600
QY 601 LSEAEVRQHREARPAALLTSRLFIKPDGLRPIVNMVYVGARTFRREKRAERLTSRVKA 660
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QY 781 QETSLRDAVIEQSSSNEASSGLFDVFLRFMCHHAVRIRGKSVYVQCQIGIPQGSILSTL 840
Db 781 QETSLRDAVIEQSSSNEASSGLFDVFLRFMCHHAVRIRGKSVYVQCQIGIPQGSILSTL 840
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Db 841 LCSLCYGMENKLFAGIRRDGLLRVDDFLVPLPHLTHAKTFLRTLVRGVPEYGCVVNL 900
QY 901 RKTVMNPFVEALGGTAFVQMPAHGLFPWCGLLDDRTLEVOQSDYSYARTSIRASLTF 960
Db 901 RKTVMNPFVEALGGTAFVQMPAHGLFPWCGLLDDRTLEVOQSDYSYARTSIRASLTF 960
QY 961 NRGFKAGNMRRKLFVLRUKCHSLFDLDQVNSLQVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNMRRKLFVLRUKCHSLFDLDQVNSLQVCTNIYKILLQAYRFHACVLQLP 1020
QY 1021 FHOQWKNPTFRLVIGDTSASLCSYLKAKNAGSLGAKAGPLSEAVOMLCHOAFLL 1080
Db 1021 FHOQWKNPTFRLVIGDTSASLCSYLKAKNAGSLGAKAGPLSEAVOMLCHOAFLL 1080
QY 1081 KLTHRVTVYVPLLSLRTAQTLRSKLPGLTTLTALEAANAAPALPSDFKTILD 1132
Db 1081 KLTHRVTVYVPLLSLRTAQTLRSKLPGLTTLTALEAANAAPALPSDFKTILD 1132

RESULT 2
telomerase reverse transcriptase - Arabidopsis thaliana
N;Alternate names: protein F5E19_190
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51517
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; New
submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25394
A;Accession: T51517
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1123 <SAT>
A;Cross-references: UNIPROT:Q9SPU7; EMBL:AL391147
A;Experimental source: cultivar Columbia; BAC clone F5E19
C;Genetics:
A;Map position: 5
A;Introns: 100/3; 125/3; 185/1; 300/3; 325/1; 369/2; 414/3; 765/3; 942/2; 1033/2
A;Note: F5E19_190

Query Match 12.2%; Score 724.5; DB 2; Length 1123;
Best Local Similarity 23.8%; Pred. No. 3.2e-41;
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Matches 294; Conservative 199; Mismatches 511; Indels 233; Gaps 39;
QY 1 MPRAPRCRAVRSLLRSHYREVLPATFV-----RRLGPOQWR-----L 38
Db 1 MPRAPRHRVPEILLWRLFGNARNLNDIAI VDLINPNRIQPEQCRGCGCLGSSDKPAFL 60
QY 39 VQRGDDPAAPFALVAQCLVCVPMDARPPAPSPFRQVSCIKELVARVLQRL---CERGAKN 95
Db 61 LRSDDPPIHYRKLHRCFV-VLHEQTPLDPSFTSMWSQREI VERIEMQSGCD--CQN 117
QY 96 VLAFFGAFALDARGGGPEAFTTSVRSYLNTVTDALRGSGAMGLLRLRRVGDVVLHLLAR 155
Db 118 VICARYDKYQS-----SPILELLT-SSWEFLKURGHVDMVYLLQ 159
QY 156 CALFVLVAPSCAVQVCGPPLYQLGAAT-----QARPPPHASGPRRRRLGCERAWNSHVS 209
Db 160 TSIFLPLLGKHOQVSGPPLCIKHKTLSVHENKRKRDNDVQPTTKROWLSSAVDDCPKD 219
QY 210 AGVPLGLPAG---ARRGGASRSLPLPKPRRGA-----APEPERTVVGGSWA 257
Db 220 DSATI-TPIVGEDVDQHREKTKTKRSRIYLKRRRKQRYNFKKVDNCNAPCITP----- 271
QY 258 HPGRTGPGSDRGFCVVPSPAPAEAEATSLGALSGTRHSHPSVGRQHAGPSTSRPRPW 317
Db 272 ---STNGKYSTG-----NDENMLHIGINGSLTDFVKQAKQ----- 303
QY 318 DTPCPPVYAEKHPLYS-SGDKEQLRPSFLLSLRPSLTGARRLVETIFLGRPMMPGTP 376
Db 304 -----VKRNKNFKFGLSETYSVIPPNHILKTRPNCSDSKLLNMHIFGEVNVMTTSP 356
QY 377 RRLPRLPQ---RYQWRPFLFLELLGNHACQPGVLLKTHCP-----LRAAVTPAAG 424
Db 357 HGKNGCPSSGICLYHSLLKSLKNLIGKTKYSSHLKMLDKHCBVLLQEDALKSGTSSOSS 416
QY 425 VCAREK-----POGSVAA-----PEEDTDPRLRLVQLLRQSHSPQVYGFVRACLRRLVPPG 476
Db 417 ---RRQKADKLPHGSSSSGTGPKCPSVEERKL-----YCTNDQVVSFIWALCRVIVES 468
QY 477 LWGSRHNERFRLNTKFTSLGKHAKLSLOELTWKMSVDCAWLRSPGVGCPAAEHLRL 536
Db 469 LUGTTHQWRVURKNIANFVSRNRNEKCTVNQFLHKVPKSDPFPFARKE--LCCMVNNGHEL 526
QY 537 REE-----ILAKFLHLMMSVVVVELLSRFFVYVTTTFOKNRFFFYRKSVWSKQSIG 588
Db 527 QSESIRSTQOMLCTKWISWLFLEIVKLVHNFVFATESQGGRLNIYYIRKSWERLISKE 586
QY 589 IRQHLKRVQLRELSAEVROHREARPAALLTSRLRPIKPDGLRPIVNMVYVGARTFRRE 648
Db 587 ISKALDGYVLVDAAESSRKK-----LSKFRFLPKANGVRMYLD-----FSSS 630
QY 649 KRAERLTSRVKALPSVLNYSERARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPP-PELY 707
Db 631 SRQSGL-----RDTTHAVLKDIQLKEPDLVGLSVDFDHDFFYRLNCPYLILHRSQSGELPPLY 686
QY 708 FVKVDVTGAYDTIPQDRLTEVIASIIKQNTYCVRRYAVVQAAHGH-----VRKAFKS 761
Db 687 FVADVPKAFSDVQGLLHVLIQSFLEKDE--YILNRCFLVCCGRKSNWVWVILVSSDKNS 744
QY 762 HVSITLTDLOPYMROFVAHLQETSPRLDAVIEQSSSNEASSGLFDVFLRFMCHHAVIR 821
Db 745 NPSRFTSTVPYNA-----LQ-----SIVVDKGENHRVKKDLMWVITGNKMLKNMLQLD 792
QY 822 GKSYYVQCQIGIPQGSILSTLCSLCYGMENKLPAGI-----RRDGL----- 862
Db 793 KSFVQIAGIPQGHRLSSLLCCFYGHLETLIYPIFEEASKOVSSKECSREELIIPTS 852
QY 863 --LLRLVDDFLVTPHITHAKTFLRTLVRGVPEYGCYVNLKRTVNVNPFVEDE----- 912
Db 853 YKLLRFIDDLVFTSRTDQASSFVHRLKHGFKDYNCFMNETKFCINFEDKEHRCSNRM 912
QY 913 --ALGGTAFVQMPAHGLFPWCGLLDDRTLEVOQSDYSYARTSIRASLTLNRFKAGNM 970
Db 913 FVGNDGVDFVR-----WTGLLINSRTFEVDYTRYLSGHSISSTFSFSAWQNKVPRNL 964
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R;Du, Z.  
submitted to the EMBL Data Library, February 1995  
A;Description: The sequence of *S. cerevisiae* cosmid 8543.  
A;Reference number: S53390  
A;Accession: S53396  
A;Molecule type: DNA  
A;Residues: 1-884 <DUZ>  
A;Cross-references: UNIPROT:Q06163; EMBL:U20618; NID:g2258165; PID:g62136; GSPDB:GN0001  
A;Experimental source: strain S288C (AB972)  
C;Genetics:  
A;Gene: SGD:EST2; MIPS:YLR318W  
A;Cross-references: SGD:S0004310; MIPS:YLR318W  
A;Map position: 12R

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Query Match          6.0%; Score 356.5; DB 2; Length 884;
Best Local Similarity 22.1%; Pred. No. 3.1e-16;
Matches 167; Conservative 127; Mismatches 309; Indels 151; Gaps 28;

Qy 329 KHFLYSGDKEQLRPS--FLLSLRPSLTGARRLV---ETIFLSGRPMWPGTPRRRLPLP 383
Db 185 KQFLH---KLININSSFFPYSKILPSSSIKKLTDLREALF-----PTNLVKIP 230
Qy 384 QRYQWMEPLFLE-LLGNHAQCPYGLKTHCPLRAAVTPAAGVCAREKPGQSVAAPEED 442
Db 231 QRLKVRINLTQLKKLKHRLNYVSIINSLCP-----PLEGTVL----- 269
Qy 443 TDPRLVQLLRQHSPPWQYGFVRACLRRLVPPGLMGSRHNERFLNTRKKFISLGRHAK 502
Db 270 ----DLSHLSNQ--SPKERVLFIIIVLOKLLPOEMFGSKNKGKIIKNLNLISLPLNGY 324
Qy 503 LSLQELTWKMSVRDCAWLRSPGVCVPAAEHLRL--EEILAKFLHLMMSVYVELLRSF 560
Db 325 LPFDSLLKRLKLDKDFWL---FISDIWFTKHNFENLNQLAICFISWLFQLPIKIIQTF 380
Qy 561 FYVTETTFQKNRLFYFKSVMSKLSIGIRQLKRVQLRELSEAEV--RQREARPAALT-- 618
Db 381 FYCTEIS-STVTIYFRHDTWNKLTITPFIYEYFKTY-----LVENNVCNRHNSYTLNFNH 435
Qy 619 SRLRFIPKPLRPIVNMVYV-----GARTFRREKRAERLTSRVKALFSLVNYERARR 672
Db 436 SKWRIIPKS-----NNEFRIIAIPCGADEEFTYIKENHKNAIQTKILEYLRNKR 489
Qy 673 PGLLGASVLGLDDIHRARWTFVLRV--RAQDPPPELYFVKVDVTGAYDTIPQDRLTRVIA 730
Db 490 PTSP-TKIYSPTQIADRIKEFKORLLKFNVLPELYFMKFDVKSCYDSIPRMECMRLK 548
Qy 731 SLIKPQNTYCVRRYAVVQKAAHGHVRKAPKSHVSTLTDLQPYMRQFVAHLQETSPLRDV 790
Db 549 DALKNENGFFVRSQYFFN--TNTGVKLKF-NVNVNASRVPKPY-----EL 589
Qy 791 VIEQSSSLNEASSGLFDVFLRFMCHHAAVRIRGKSYVOCQIPQGSIIILSTLLCSLCYGD- 849
Db 590 YIDNVRTVHLSNQDVINNVEMEIPKTAIWEDKCYIREDGLFQSSLSAIVDLVYDDL 649
Qy 850 --ENKLPAGIRRDGLLRLLVDFLLVTPHILTHAKTFLRTLVRGVPYEGCVVNLRKTV-VN 906
Db 650 EYSEFKASPSQDTLLKLDADDFLIISTDQOQVINIKKLAMGGFQKYNANAKNRDKILAVS 709
Qy 907 FPVEDEALGTAFAVQMPAHGLFPWCGLLDTRTLEVDSDYSSYARTSIRASLTFNRGFK 966
Db 710 SQSDDDT-----VIOFCAMHI FVKELEVWKSSTMNPHIRS-----KS 748
Qy 967 GRNMRRKLFGLRLKCHSLFDLDQVNSLQVCTNI-----YK-----ILLQ 1009
Db 749 SKGIFRSLIALFNTRISYKTIIDTNLNTNLTVMQIDHVVKNISCYKSAFKDLSINTQN 808
Qy 1010 YRFHACVLQLPFHQOVKNPTFFLRVLSIDTASLC 1043
Db 809 MQFH-----SFLQRIIEMTVSGC 826
```

RESULT 7  
A59266

```
unconventional myosin-15 - human
C;Species: Homo sapiens (man)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: A59266
R;Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.;
an, T.B.; Fridell, R.A
Genomics 61, 243-258, 1999
A;Title: Characterization of the human and mouse unconventional myosin XV genes respons
A;Reference number: A59266; MUID:20021762; PMID:10552926
A;Accession: A59266
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-3530 <LIA>
A;Cross-references: UNIPROT:Q9UKN7; GB:AF144094; NID:g6224682; PIDN:AAF05903.1; PID:g62
F;1225-1887/Domain: myosin motor domain homology <MWO>

Query Match          3.0%; Score 176.5; DB 2; Length 3530;
Best Local Similarity 20.6%; Pred. No. 0.0041;
Matches 263; Conservative 144; Mismatches 392; Indels 475; Gaps 68;

Qy 107 ARGGPPEAFTTS-----VRSYLP-----NTVTDALRGSGAWG 138
Db 2313 SRGGPKVVFNGNSDEDMSSTRPQPEHMPKVLDSDGYSSHNDQGTNGETEAOQGT-ATH 2371
Qy 139 LLRLRRGDDVLVHLLARCALFVLVAP-----SCAYQVCQPPILYQLGAA---- 181
Db 2372 QESDSLGEPAVPHKGLDCLDLSLDFPVLVSYGDADLEKPTAIAYRMKGGQPGGGSSGTE 2431
Qy 182 -TQARPP---PHASGPRRLGCRANVHVSREAGV---PLGLPAPARRGGSSAS-RSLP 233
Db 2432 DTPRRPEPPKPIPLDASTLALQQAFTH--KQAVLLARGMTLQATALQQPPLSAAALSLP 2489
Qy 234 LPKRRRGAAPERTPVGOGSWAHQPTRGPSDRGCVVSPARPASEATSEALSGSTR 293
Db 2490 AEKPP-----APEAQPTSVGTGPPAKPVLLR-----ATPKPLAPA----- 2524
Qy 294 HSHPSVGRQHHAGGPPSTSRPPRPMWTPCPPIYA-----ETKHFLYSSGKEQLRPSFLL 347
Db 2525 -----PLAKAPRLPIKVAAPVLAQDOQASPET-----TSPSELVRYSTLN 2565
Qy 348 SSLRPSLTGARRLVEIFLGSRRPMWGTTPRLRLPQRYWQMRP-----LFEILGNH 400
Db 2566 SEHFPOPT--QQIKNIVRQYQQPFRGGRPEALRKDGKVKPMKPPDPHEEALMLKGMTH 2623
Qy 401 AQCPYG-----VLLK--THCPLRAAVTPAGVCAREKPGQSVAAPEE-EDTDPRRLV 449
Db 2624 LAAPGTQVGREAVLVKPVTSAP-RPSMAPTSAI-----PSRSLPEPELTQTRLRLRI 2677
Qy 450 --QLLRQHSPPWQYGFVR-----ACLR-----RL 472
Db 2678 NPNFYGQDAPWKI--FLRKEVFYPKDSYSHVPVQLDLPRQILHDLTLSEACLRISEDRL 2735
Qy 473 VPPELGMSRINERFLNTRKKFISLG-KHAKLSLQELTWKMSVRDCAWLRRSPGVCVPA 531
Db 2736 RMKALFAQNO-----LDTQKPLVTESVKRAVWSTARDTWEV-----YFSRIFPATGSGVT 2785
Qy 532 AEHLREELAKFLHLMMSVYVELLR-----SPFYVTETTF-QKNR 572
Db 2786 G-----VQLLA-----VSHVGIKLLRMVKGQEGAGQLRVLRAYSADILFTVMPSONM 2834
Qy 573 LFFYRKSVMSKLSIGIRQLKRVQLRELSEAEVRQHRREARPAALLTSRLRFIPKPDGLRP 632
Db 2835 LEFNLAS--EKVILFSARAH---QVKTLVDDDFILELKK----- 2867
Qy 633 IVNMDYVVGARTPRRKRABERLTSRVKALFSLVNYERA-----RRPGLLGAS----- 679
Db 2868 --DSDYVAVARNFLPBDPA-----LLAFHKGDIIHLQPLEPPRPGVYSAGCVVR 2913
Qy 680 --VLGLDDIHR-----AWRTFVLVRQAQDPPPELYFVKVDVTGAYD-----TIP-QDRLT 726
Db 2914 RKVVYLEELRRRGDFGWRFGTTHGRVGRPPSEL-----VQPAAPDFLQPTBPGRRAA 2969
Qy 727 EVIASIIPQNTYCVRRY-----AVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQ 781
```

```
Db 2970 AVAAAVASAAAEVGRRRREGPPVRRASADHGEDALALPPY-TLFEFAQKYFRDPQRRPQ 3028
QY 782 E-----TSPLRDAVIEOSSSLNEASSGLDFVFLRFMCHHAVR 819
Db 3029 DGLRLKSKPRSRRTLEDMLCTKTPQLQSLIELSDSSLSKXWATDMFLAVRMFGDAPLK 3088
QY 820 IRKSVVOCGIPQGSILSTLLCSLCYGD---MENKLFAGI-----RRDG 861
Db 3089 GQSDLDVLCN-----LLKLC-GDHEVWRDECYQVVKQITDNTSSKQSPCQGW 3136
QY 862 LLRLRVDDF-----LLVTPHLTHAKTFLRLVR--GVPEYG-----CVNLRKTVVNFVVED 911
Db 3137 RLIIYIVTAVHSCSEVLHPLHTR---FLODVSRTPGLFPFGIAKACEQNQLKTL----- 3186
QY 912 EALGGTAFVQMPAHGLFPMCGLLDTRTLEQSDVSSVARTSIRASLTFNRFAGRNMR 971
Db 3187 -RFGG-----RLELPSS-----TELRLM-----AGRSSK 3210
QY 972 RKLK-----GV-----LRKCHSLFLDLQVNSLQTVCT-----NIYKILLQAYRPHA 1014
Db 3211 ROLFLLPGGLERHLKIKTCTVALDV---VEEICAEMALTRPEAFNEVIFVVTNRQGV 3266
QY 1015 CVL-----QLPFHQVQWKPTFF-----LRVISTASLCY 1044
Db 3267 CPLSRRAVLDAVASEMEQVGGYMLWFRRLVLDQPLKFENELYVTMHNQVLPDYLKGLF 3326
QY 1045 SILKAKNAGMSIGAKGAGPLPSEAVQWLCHQAFLLKLTTRHVT---YVPLLSLRTAQ-- 1100
Db 3327 SSVPASR-----PSEQ---LLOQVSLASLQHRAXDHFYLP---SVREQE 3366
QY 1101 ---TQLSRKLPGTT 1111
Db 3367 YIPAQLYRTTAGST 3380

RESULT 8
QBHE3
BHLF1 protein - human herpesvirus 4 (strain B95-8)
C:Species: human herpesvirus 4, Epstein-Barr virus
C>Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
C:Accession: A03742
R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A>Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
A:Reference number: A93065; MUID:85035713; PMID:6092825
A:Molecule type: DNA
A:Accession: A03742
A:Residues: 1-660 <BAN>
A:Cross-references: UNIPROT:P03181
R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
Nature 310, 207-211, 1984
A>Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A:Reference number: A03794; MUID:94270667; PMID:6087149
A:Contents: annotation: protein coding region
C:Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, 399-52
C:Superfamily: human herpesvirus 4 BHLF1 protein

Query Match 2.9%; Score 172.5; DB 1; Length 660;
Best Local Similarity 26.1%; Pred. No. 0.00078;
Matches 94; Conservative 16; Mismatches 159; Indels 91; Gaps 16;

QY 167 AYQVC-GPPYLQGAATQA-RPPHAGSPRRRLGCERAWNHSVREAGVPLGLPAPGAR 222
Db 244 AAQRCFAGPPPTTSGAAQRTTHRRPPGCPRSARNPGCPRTWR---RRSGAQRGHPPPGAG 300
QY 223 RRGGSASRLP-LPKRPRGAPEP-ERTPVGGGWAHPQRTGSDRGFCV-VSPAR-- 277
Db 301 QRPSTGGRPAAPGAPGTPAAPGGGAAVPSGATPHPERGSGPADPPAARLPPERQE 360
QY 278 -----PABEATSELEGAL-----SGTRHSHP 297
Db 361 PRLPDLLAAQRCFAGPPPTTSGAAQRTTHRRPPGCPRSARNPGCPRTWRRRSGAQRGHP 420
```

```
QY 298 SVGRQHAGPPSTSRPRPW--DTPCPP-----VYAEKHFLYSSGDK-----QLR 342
Db 421 PPGAGQRPSTGTRPAAPGAPGATPAAPGGGAAVPSGATPHPERGSGPADPPAARLP 480
QY 343 PSFLLSLRSLGARRLVETIFLGRPMWPG-----TPRRLRLPQ-----RYQM 389
Db 481 PERQEPRLPDLLAAQRCF-----AGPPPTTSGAAQRTTHRRPPGCPRSARNPGCPRTWR 536
QY 390 RPLFLELLGNHQAOCFYGLLKTHCPL--RAAVTPAAGVCAREKPGQGSVAAPBEEDTPRR 447
Db 537 RS-----GAQRGHPHPPGAGQRPSTGTRPAAPGATPAAPGGGAAVPSGATPHPER 591

RESULT 9
A59295
unconventional myosin-15 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59295
R:Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probat, F.J.; Barber, T.D.; M;
an, T.B.; Fridell, R.A.
Genomics 61, 243-258, 1999
A>Title: Characterization of the human and mouse unconventional myosin XV genes respons
A:Reference number: A59266; MUID:20021762; PMID:10552926
A:Accession: A59295
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-3511 <LIA>
A:Cross-references: UNIPROT:Q9QZ24; GB:AF144095; NID:G6224684; PIDN:AAF05904.1; PID:G62
C:Genetics:
A:Gene: MGI:Myo15
A:Cross-references: MGI:1261811
A:Map position: 11:33.9
F:1209-1871/Domain: myosin motor domain homology <MMO>
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Query Match 2.4%; Score 144; DB 2; Length 3511;
Best Local Similarity 17.6%; Pred. No. 0.68;
Matches 189; Conservative 117; Mismatches 385; Indels 380; Gaps 44;

QY 3 RAPRCRAVRSLLRSHYREVLPATFVRLRGPGQWRLVQRGDPAAFRALVAOCLVCVP-- 59
Db 677 RPPRLASPYGSLRQH-----PPW-----AAAHVFFPPQA 707
QY 60 --WDARPPAA-----PSFQVSCLELVARVLCERGAKNVLAFGA 102
Db 708 NWMGFAEPPTGSEVAPDLLAPPVPRPSFR-----ASRSRSRAAYGFP 751
QY 103 LLDGARGPPEAFTTSVRSYLPNTVTD--ALRGSAGWLLLRVDDVVLHLLARCALFV 160
Db 752 -----SPSLIGSRRRPHLPSPQSLRSLPGQG----- 778
QY 161 LVAPSCAVQVCPPYLQGAATQARPPHAGSPRRRLGCERAWNHSVREAGVPLG----- 215
Db 779 -----YHSLPLGLSPQLSLRGRFPQFPFPPRRPQSLREAF--SLRRASGRGLGPPRSP 830
QY 216 -----LPACARRRGSGASRSLPLPKR-----PRGAAPEPPT--PVQGS 255
Db 831 VLGSFRPPSPPLLKHGFRHRSNLPLSLRPLRTWRRLSEPPTRAVKPWVHRAYPPPSAGP 890
QY 256 WAHPGRTGSDRGFCVVSAPPAEATSLGALSGTRHSHPSVGRQHAGPPSTSRPR 315
Db 891 W---GASTGALE-----QENQREADESETPTWTPPLPSWDVMDPPTQPPS 935
QY 316 PWDTPC-----PPVYAEKHFLYSS-----GDKEQLRPSFLS 348
Db 936 FWPEGIGSLRGFRPPPPVPENPLEHTSPSCPEQSDRVSNLTGIFLGQHHDPGCGLT 995
QY 349 SLRPSLTGARRLVETIFLGRPMWPGTTPRL--PRLPQRYWQMPLFLLELGNH----- 400
Db 996 SADSPL---EKPEVTVLGD--POPPAEPEALNTPFNKNVSVSRKVLRLSASVPLVTCQ 1051
QY 401 --AQCP-----YGVLLKTHCPLRAAVTPAAGVCAREKPGQS----- 434
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Qy 338 KEQLRPSFLSLSLGARRLVETIFLGSRPWMPG-TPR-RL-PRLPQRYWQMRPLFL 394
Db 182 EPRTR- ---LQPATPRRSGAADPADPVGHAPRAPGPEPRTRLQPATPRRSGAADP--A 235
Qy 395 ELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPGSGSVAAPDEEDTDPRRLVQ 450
Db 236 DFIG-HPAAPRAPGPEPRTRLQPATPRRSGAADPADPVGHAPRAPGPEPRTRLQ 290

RESULT 15
C45219
N-methyl-D-aspartate receptor chain NMDAR2D-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: C45219
R:Ishii, T.; Moriyooshi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, M.; Akazawa
J. Biol. Chem. 268, 2836-2843, 1993
A:Title: Molecular characterization of the family of the N-methyl-D-aspartate receptor
A:Reference number: A45219; MUID:93155102; PMID:8428958
A:Accession: C45219
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1356 <ISH>
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBIP:124264)
C:Superfamily: N-methyl-D-aspartate receptor 2D; glutamate receptor homology
F:451-879/Domain: glutamate receptor homology <GRH>

Query Match 2.3%; Score 135; DB 1; Length 1356;
Best Local Similarity 27.2%; Pred. No. 0.76;
Matches 88; Conservative 16; Mismatches 102; Indels 118; Gaps 22;

Qy 59 FWDARPPPPAA-----PSFRQVSCLELVARVLQRCERGAKNVLAFGFALLDG----- 106
Db 1084 PRRAAPPCAYLDLEPS-----PSDSEDSLSLGGASLGGLPEWFA 1124
Qy 107 -----ARGGPEAFTTSVRSYLPNTVTDALRG--SGANGLLLRVGGDDVLVHLLARCA 157
Db 1125 DFYPYAERLGPPPGRYMSV-----DKLGGWRAGSDYLPFRGGP---AWHCRHCA 1172
Qy 158 LFVLVAP-----SCAYQVC-----GPPLYQLGNAQTQARPPPHASGP-----RRRLGCERAWN 204
Db 1173 SLELLPPRHLSCSHDGLDGGWAPP-----PPWAGPPPPRRRARCPCPRPH 1221
Qy 205 HSVREA-GVPLGLPAGARR--GG-----SASRSL-PLPKPRRGAAPEPERT-PVG 252
Db 1222 HRPRASHRAPAAAPHHHRRRAAGWDPPFPAPTSSLEDLSRP-----CP-PHRTGDTG 1276
Qy 253 QGSWAHPGRTGPSDRGFCVVSP-----ARPAEATSLEGALSGTRHSHPSVGRQHHA 305
Db 1277 AGTWAHAGALR-----ISPAWSPRYDAAPAPTPTPAAPSVSA---GHGPRGAKWT 1324
Qy 306 GPPSTSR-----PPR--PWDTCPP 323
Db 1325 GPSWVGKDRNGFGRTPPGAASCAP 1348
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Search completed: January 10, 2005, 17:39:30  
Job time : 57 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 10, 2005, 17:19:31 ; Search time 168 Seconds  
(without alignments)  
2417.152 Million cell updates/sec

Title: US-10-053-758-225

Perfect score: 5961

Sequence: 1 MPRAPRCRAVRLSLRSHYRE.....TALEAAANPALPSDFKTLTD 1132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 200273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A\_Geneseq\_23Sep04:\*
- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	1132	2	AAW46957 Human tel
2	5961	100.0	1132	2	AAW90251 Human cat
3	5961	100.0	1132	2	AAV28881 Human tel
4	5961	100.0	1132	2	AAV32090 Human tel
5	5961	100.0	1132	2	AAV43621 A human t
6	5961	100.0	1132	2	AAV26580 Human tel
7	5961	100.0	1132	4	AAV64859 Heart mus
8	5961	100.0	1132	4	AAV64329 Human pro
9	5961	100.0	1132	4	AAV99930 Human tel
10	5961	100.0	1132	4	AAV82765 Human tel
11	5961	100.0	1132	5	AAE29226 Human tel
12	5961	100.0	1132	5	AAU72735 Human tel
13	5961	100.0	1132	6	ABR42384 Human tel
14	5961	100.0	1132	6	ABR42063 Human tel
15	5961	100.0	1132	6	ABP56676 Human tel
16	5961	100.0	1132	6	ABR58045 Human tel
17	5961	100.0	1132	7	ADD21420 Human TER
18	5961	100.0	1132	7	ADH72743 Human pro
19	5961	100.0	1132	8	ADG70114 hTERT pro
20	5961	100.0	1132	8	ADG90599 Human TER
21	5961	100.0	1132	8	ADI82172 Human tel
22	5961	100.0	1154	2	AAW61350 Human tel
23	5961	100.0	1189	2	AAW47008 Glutathio
24	5955	99.9	1285	2	AAW47000 HIS tagge
25	5954	99.9	1132	2	AAW71376 Human tel

26	5954	99.9	1132	2	AAV00627 Human tel
27	5954	99.9	1132	2	AAV00638 Truncated
28	5954	99.9	1132	2	AAV28401 Human EST
29	5954	99.9	1132	3	AAV96566 hEST2, a
30	5954	99.9	1132	7	ADG47061 Human TER
31	5954	99.9	1132	7	ADG40482 Human tel
32	5952	99.8	1132	2	AAW56113 Human tel
33	5927	99.4	1166	2	AAV00647 Telomeras
34	5918	99.3	1405	2	AAW56101 Enhanced
35	5911.5	99.2	1199	2	AAW47007 Glutathio
36	5882	98.7	1120	2	AAV00641 Telomeras
37	5873	98.5	1120	2	AAV00650 Telomeras
38	5721	96.0	1150	2	AAW47006 Glutathio
39	5555	93.2	1053	2	AAV00640 Altered C
40	5516	92.5	1093	2	AAV00649 Altered C
41	5467	91.7	1041	2	AAV00652 Altered C
42	5467	91.7	1041	2	AAV00643 Altered C
43	5008	84.0	948	2	AAV00639 N-termina
44	5004	83.9	948	2	AAV00648 Truncated
45	4932	82.7	936	2	AAV00642 Truncated

ALIGNMENTS

RESULT 1

AAW46957  
ID AAW46957 standard; protein; 1132 AA.

XX AC AAW46957;

XX DT 73-AUG-1998 (first entry)

XX DE Human telomerase reverse transcriptase.

XX HW Human; telomerase reverse transcriptase; hTERT; TRF; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.

XX OS Homo sapiens.

XX PN 6B2317891-A.

XX PD 08-APR-1998.

XX PF 01-OCT-1997; 97GB-00020890.

XX PR 01-OCT-1996; 96US-00724643.

XX PR 18-APR-1997; 97US-00844419.

XX PR 25-APR-1997; 97US-00846017.

XX PR 06-MAY-1997; 97US-00851843.

XX PR 09-MAY-1997; 97US-00854050.

XX PR 14-AUG-1997; 97US-00911312.

XX PR 14-AUG-1997; 97US-00912951.

XX PR 14-AUG-1997; 97US-00915503.

XX PA (GERO-) GERON CORP.

XX PA (UYTE-) UNIV TECHNOLOGY CORP.

XX PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB; Andrews WH;

XX PT WPI; 1998-171633/16.

XX DR N-PSDB; AAV22379.

XX XX Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.

XX PS Claim 3; Fig 17; 387pp; English.

XX CC The present sequence represents human telomerase reverse transcriptase (hTERT), which is a ribonucleoprotein. The present invention also describes the following methods: (A) determining whether a test compound

CC is a modulator of hTERT, by detecting the change in hTERT recombinant  
 CC protein or polynucleotide, on administration of the compound; (B)  
 CC preparation of recombinant telomerase by contacting a protein preparation  
 CC of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or  
 CC protein in a sample by binding a relevant probe to the sample and  
 CC detecting the complex formed or in the case of RNA detection, amplifying  
 CC the product and correlating the presence of complex or amplification  
 CC product with presence of hTERT in the sample; and (D) increasing the  
 CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)  
 CC the use of an agent that causes an increase in cell vertebrate cell  
 CC proliferation to create a medicament that inhibits ageing. A protein  
 CC preparation of hTERT and the polynucleotide encoding hTERT can be used in  
 CC the manufacture of medicaments for inhibiting the effect of ageing or  
 CC cancer. Inhibitors of telomerase activity can be used to treat conditions  
 CC that are associated with high telomerase activity. A protein preparation  
 CC of hTERT can also be used in the new methods

XX  
 SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQGDPAAPRALVAQCLVCVPW 60  
 DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQGDPAAPRALVAQCLVCVPW 60

QY 61 DAPPPAAPSFRQVSCLEKELVAVLQRLCERGAKNVLAFCGALLDARGGPPFAFTSVR 120  
 DB 61 DAPPPAAPSFRQVSCLEKELVAVLQRLCERGAKNVLAFCGALLDARGGPPFAFTSVR 120

QY 121 SYLPNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYOCVGPPLYLQGA 180  
 DB 121 SYLPNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYOCVGPPLYLQGA 180

QY 181 ATQARPPPHASGRRRLGCRANVHSVREAGVPLGLPAGCARRRGSASRSLPLKPRRR 240  
 DB 181 ATQARPPPHASGRRRLGCRANVHSVREAGVPLGLPAGCARRRGSASRSLPLKPRRR 240

QY 241 GAAPERTPVGGSWAHPTGSDRGFCVUSPARPAEATSLGALSGTHSPSVG 300  
 DB 241 GAAPERTPVGGSWAHPTGSDRGFCVUSPARPAEATSLGALSGTHSPSVG 300

QY 301 ROHAGPPSTSRPRPDWTPCPVYAEKTHFLYSSGDKQOLRPSFLLSLRPLSGTARRL 360  
 DB 301 ROHAGPPSTSRPRPDWTPCPVYAEKTHFLYSSGDKQOLRPSFLLSLRPLSGTARRL 360

QY 361 VETIFLGSRPMPGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420  
 DB 361 VETIFLGSRPMPGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEEDTPRLVOLLROHSPQWYGVFVRACLRLVPPGLWGS 480  
 DB 421 PAAGVCAREKPGQSVAAPEEEDTPRLVOLLROHSPQWYGVFVRACLRLVPPGLWGS 480

QY 481 RHNERFRNTRKXIFSLGKHAKLSLOBLTWKMSVRDCAWLRSPGVCVPAAEHRLRESI 540  
 DB 481 RHNERFRNTRKXIFSLGKHAKLSLOBLTWKMSVRDCAWLRSPGVCVPAAEHRLRESI 540

QY 541 LAKFLHLMVSVYVELLRFFYVTTTFOKNRFFYRKSVWSKLQSIGIRQHLKRVQVRE 600  
 DB 541 LAKFLHLMVSVYVELLRFFYVTTTFOKNRFFYRKSVWSKLQSIGIRQHLKRVQVRE 600

QY 601 LSAEVRQREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFREREKRELTSRVKA 660  
 DB 601 LSAEVRQREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFREREKRELTSRVKA 660

QY 661 LFSVLNYSARRPGLLGASVLGDDIHRARWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720  
 DB 661 LFSVLNYSARRPGLLGASVLGDDIHRARWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720

QY 721 PQDRLTEVIASIIKPNTYCVRRYAVVQKAAHGHVKAFAKSHVSTLTLDLPQYMRQFVAHL 780

DB 721 PQDRLTEVIASIIKPNTYCVRRYAVVQKAAHGHVKAFAKSHVSTLTLDLPQYMRQFVAHL 780  
 QY 781 QETSPLRDAVVIQSSSLNEASSGLDFVFLRFMCHHAVIRGKSYVQCQIGIPQGSILSTL 840  
 DB 781 QETSPLRDAVVIQSSSLNEASSGLDFVFLRFMCHHAVIRGKSYVQCQIGIPQGSILSTL 840  
 QY 841 LCLSCYGDGMENKLFAGIRDRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900  
 DB 841 LCLSCYGDGMENKLFAGIRDRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900  
 QY 901 RKTVMNFPVEDBALGTAFAVQMPAHGLFPWCGLLLDRTLLEQVSDYSSVARTSIRASLTF 960  
 DB 901 RKTVMNFPVEDBALGTAFAVQMPAHGLFPWCGLLLDRTLLEQVSDYSSVARTSIRASLTF 960  
 QY 961 NRGFKAGRNRRKLFQVLRKCHSLPLDLQVNSLQVCTNIYKILLLOAYRHACVQLQP 1020  
 DB 961 NRGFKAGRNRRKLFQVLRKCHSLPLDLQVNSLQVCTNIYKILLLOAYRHACVQLQP 1020  
 QY 1021 FHQQVWKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080  
 DB 1021 FHQQVWKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080  
 QY 1081 KLTRHRVTYVPLLGSLRTAQTOLSRKLPOTTLTALAAANPALPSDFKTILD 1132  
 DB 1081 KLTRHRVTYVPLLGSLRTAQTOLSRKLPOTTLTALAAANPALPSDFKTILD 1132

## RESULT 2

AAW90251  
 ID AAW90251 standard; protein; 1132 AA.  
 XX  
 AC AAW90251;  
 DT 24-MAY-1999 (first entry)  
 XX  
 DE Human catalytic telomerase sub-unit protein.  
 XX  
 KW Human; catalytic telomerase subunit; therapy; diagnosis; hTC; assay;  
 KW modulator; treatment; inhibit; cellular disorder; death; defect; cancer;  
 KW ageing; antisense; neoplastic cell; telomerase-related condition;  
 KW tumour cell.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9859040-AZ.  
 XX  
 PD 30-DEC-1998.  
 XX  
 PF 09-JUN-1998; 98WO-EP003468.  
 XX  
 PR 20-JUN-1997; 97DE-01026329.  
 PR 26-MAR-1998; 98DE-01013274.  
 PR 14-APR-1998; 98DE-01016496.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 PI Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;  
 XX  
 DR WPI; 1999-081276/07.  
 DR N-PSDB; AAV72117.  
 XX  
 PT New catalytically active subunit of human telomerase - used in the  
 PT modulation of telomerase activity, particularly for treating cancer and  
 PT ageing.  
 PS  
 PS Claim 2; Fig 2; 76pp; German.  
 XX  
 CC This sequence represents a novel human catalytic telomerase sub-unit  
 CC (hTC). This protein can be used in screening assays to identify  
 CC modulators of telomerase and to treat or inhibit cellular disorders,  
 CC death, defects and/or other pathological processes involving telomerase,  
 CC particularly cancer and ageing (also suitable for this are agents that  
 CC stimulate, inhibit or mimic the activity of the subunit). Antisense

CC nucleic acids inhibit telomerase action (by binding to specific mRNA), particularly in neoplastic cells and may be expressed in vivo. Antibodies and fragments of the protein, used as probes or primers, are used to diagnose telomerase-related conditions (especially neoplasia) by (i) detecting abnormal levels of the subunit protein in body fluids or tissues or (ii) by measuring the amount of the encoding nucleic acid. Expression of the nucleic acid encoding the subunit mRNA is confined to tumour cells, in contrast to the ubiquitous expression of the telomerase RNA subunit

XX  
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVSLRSHREVLPLATFVRRIGPGQWRLVQRGDDPAAPALVAQCLVCVPW 60  
DB 1 MPAPRCRAVSLRSHREVLPLATFVRRIGPGQWRLVQRGDDPAAPALVAQCLVCVPW 60

QY 61 DARPPPAAPSFRQVSCLEKELVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120  
DB 61 DARPPPAAPSFRQVSCLEKELVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120

QY 121 SYLNTVTDALRGSGAWGLLRRVCGDDVLVHLLARCALLFVLVAPSCAYQVCGPPLYQLGA 180  
DB 121 SYLNTVTDALRGSGAWGLLRRVCGDDVLVHLLARCALLFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATOARPPPHASGPRRLRCERAWHNSVREAGVPLGLPAGARRGGSSASRLPLPKPRR 240  
DB 181 ATOARPPPHASGPRRLRCERAWHNSVREAGVPLGLPAGARRGGSSASRLPLPKPRR 240

QY 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRISHSPVG 300  
DB 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRISHSPVG 300

QY 301 ROHAGPSTSRPPRPMDTPCPPVYAEKHFYLSGGDKQLRPSFLLSLSPSTGARRL 360  
DB 301 ROHAGPSTSRPPRPMDTPCPPVYAEKHFYLSGGDKQLRPSFLLSLSPSTGARRL 360

QY 361 VETIFLGRPMPTGTRPLRPLQRYWQMRPLFELLGNHAOCYGVLLKTHCPRLRAVT 420  
DB 361 VETIFLGRPMPTGTRPLRPLQRYWQMRPLFELLGNHAOCYGVLLKTHCPRLRAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRHSSPWQVYGFVRACLRRLVPPGLMGS 480  
DB 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRHSSPWQVYGFVRACLRRLVPPGLMGS 480

QY 481 RHNERRFLRNTKKFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCPVAAEHLRBEI 540  
DB 481 RHNERRFLRNTKKFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCPVAAEHLRBEI 540

QY 541 LAKFLHWMVYVVELLSRFPYVTTTQKRLFPYKSVWSKLSQIGIROHLKRVQURE 600  
DB 541 LAKFLHWMVYVVELLSRFPYVTTTQKRLFPYKSVWSKLSQIGIROHLKRVQURE 600

QY 601 LSEAEVROHREARPAALLTSRLRFPKPDGLPIVNMDDVVGARTFRREKRAERLTSRVKA 660  
DB 601 LSEAEVROHREARPAALLTSRLRFPKPDGLPIVNMDDVVGARTFRREKRAERLTSRVKA 660

QY 661 LFSVLNFERARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720  
DB 661 LFSVLNFERARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720

QY 721 PODRLTEVIASIIKPQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTLQPYMQFVAHL 780  
DB 721 PODRLTEVIASIIKPQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTLQPYMQFVAHL 780

QY 781 QETSPLRDVAIVEOSSLINEASSGLFDVFLFMCHAVIRIGKSVQCGIPQGSILSTL 840  
DB 781 QETSPLRDVAIVEOSSLINEASSGLFDVFLFMCHAVIRIGKSVQCGIPQGSILSTL 840

QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYEGCVNVL 900

DB 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYEGCVNVL 900

QY 901 RKTVVNFPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRSLTF 960

DB 901 RKTVVNFPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRSLTF 960

QY 961 NRGFKAGRNMRRLFGVLRUKCHSLFLDLQVNSLQTVCTNIIYKILLQAYRFHACVLQLP 1020

DB 961 NRGFKAGRNMRRLFGVLRUKCHSLFLDLQVNSLQTVCTNIIYKILLQAYRFHACVLQLP 1020

QY 1021 FHOQVKNPTFFFLRVISDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHOAFLL 1080

DB 1021 FHOQVKNPTFFFLRVISDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHOAFLL 1080

QY 1081 KLTRHRTVYVPLGLSLRTAQTOLSRKLPGTTLTALEAAANPALPSDFKTIID 1132

DB 1081 KLTRHRTVYVPLGLSLRTAQTOLSRKLPGTTLTALEAAANPALPSDFKTIID 1132

RESULT 3  
AAV28881  
ID AAV28881 standard; protein; 1132 AA.  
AC AAV28881;  
XX  
DT 17-JAN-2000 (first entry)  
XX  
DE Human telomerase reverse transcriptase protein.  
XX  
KW Human telomerase reverse transcriptase protein; hTERT; telomerase; hEST2; catalytic protein component; cell proliferative capacity; DNA primer; telomerase substrate; telomeric DNA synthesis; cell immortality; neoplastic phenotype; diagnostic application; prognostic application; telomerase related condition; cancer; therapeutic agent;  
KW telomerase expression; telomerase activity.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 608 /note= "Corresponds to cac codon"  
FT  
XX  
PN WQ950279-A1.  
XX  
PD 07-OCT-1999.  
XX  
PF 31-MAR-1999; 99WO-US007160.  
XX  
PR 31-MAR-1998; 98US-00052919.  
XX  
PA (GERO-) GERON CORP.  
PA (UYTE-) UNIV TECHNOLOGY CORP.  
XX  
PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB; Andrews WH;  
PI  
XX  
DR WPI; 1999-610834/52.  
DR N-PSDB; AAZ08150.  
XX  
PT Antisense polynucleotides for human telomerase reverse transcriptase used for diagnosing or treating cancer.  
PT  
XX  
PS Claim 2; Fig 2; 31pp; English.  
XX  
CC The present sequence is human telomerase reverse transcriptase protein. This is the catalytic protein component of telomerase and is also referred to as hEST2. hTERT has the ability to extend a DNA primer that functions as a telomerase substrate for telomeric DNA synthesis. This correlates with cell proliferative capacity, cell immortality, and the development of a neoplastic phenotype. Human hTERT antisense oligonucleotides are useful for diagnostic or prognostic applications to telomerase related conditions, including cancer. They are also useful as

CC	therapeutic agents, for inhibition of telomerase expression and activity	
XX		
SQ	Sequence 1132 AA;	
	Query Match 100.0%; Score 5961; DB 2; Length 1132;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MPRAPRCRAVRSLLRSHRYEVLPLATFVRRLLGQGMRLVORGDPAAAFRALVAOCLVCVPW 60	
DB	1 MPRAPRCRAVRSLLRSHRYEVLPLATFVRRLLGQGMRLVORGDPAAAFRALVAOCLVCVPW 60	
QY	61 DARPPPAAPSRQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120	
DB	61 DARPPPAAPSRQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120	
QY	121 SYLPTNTVDALRSGGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180	
DB	121 SYLPTNTVDALRSGGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180	
QY	181 ATQARPPPHASGPRRRLCGERAWNHSVREAGVPLGLPAPGARRRRGGASRSLELPKPRRR 240	
DB	181 ATQARPPPHASGPRRRLCGERAWNHSVREAGVPLGLPAPGARRRRGGASRSLELPKPRRR 240	
QY	241 GAAPEPERTVPGQGSNAHPQRTGPDRCFVVSPPAPAEATSLGALSSTGRHSHPSVG 300	
DB	241 GAAPEPERTVPGQGSNAHPQRTGPDRCFVVSPPAPAEATSLGALSSTGRHSHPSVG 300	
QY	301 ROHHAGPPTSRRPRPMDTCPVYAETHKFLYSSGDKKEQLRPSFLISSLRPSLTGARRL 360	
DB	301 ROHHAGPPTSRRPRPMDTCPVYAETHKFLYSSGDKKEQLRPSFLISSLRPSLTGARRL 360	
QY	361 VETIFLGSRRPWPCTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAAT 420	
DB	361 VETIFLGSRRPWPCTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAAT 420	
QY	421 PAAGVCAREKPOGSVAAPSEEDTDPRLLVQLLRQHSSPMQVYGVFVRACLRLRVPGLWGS 480	
DB	421 PAAGVCAREKPOGSVAAPSEEDTDPRLLVQLLRQHSSPMQVYGVFVRACLRLRVPGLWGS 480	
QY	481 RHNERFLRNTKFIISLGKHAQLSLOELLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEL 540	
DB	481 RHNERFLRNTKFIISLGKHAQLSLOELLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEL 540	
QY	541 LAKFLHLMVSVVVELLRSFYTTTFOKNRFFFYRKSWSKLQSIGIRQHUKRVQLRE 600	
DB	541 LAKFLHLMVSVVVELLRSFYTTTFOKNRFFFYRKSWSKLQSIGIRQHUKRVQLRE 600	
QY	601 LSAEVRQHREARPALTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKAERLTSRVKA 660	
DB	601 LSAEVRQHREARPALTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKAERLTSRVKA 660	
QY	661 LFSVLNVERARRGLLGASVLGLDDTHRAWRTFVLVRAQDDPPPELYFVKVDVTGAYDTI 720	
DB	661 LFSVLNVERARRGLLGASVLGLDDTHRAWRTFVLVRAQDDPPPELYFVKVDVTGAYDTI 720	
QY	721 PQDLRETVASIIKPNQTYCVRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780	
DB	721 PQDLRETVASIIKPNQTYCVRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780	
QY	781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRIGKSVYQCQIIPQGSILSTL 840	
DB	781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRIGKSVYQCQIIPQGSILSTL 840	
QY	841 LCSLCYGDMEKULFAGIRRDGLLRLVDDPFLVTPHITHAKTFLRTLVRGPVYGCVNL 900	
DB	841 LCSLCYGDMEKULFAGIRRDGLLRLVDDPFLVTPHITHAKTFLRTLVRGPVYGCVNL 900	
QY	901 RKTVMNPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVDSDYSSTARTSIRASLTF 960	
DB	901 RKTVMNPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVDSDYSSTARTSIRASLTF 960	
QY	961 NRGEKAGRNMRRLFGVLRLLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020	

DB	961 NRGEKAGRNMRRLFGVLRLLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020	
QY	1021 FHQQVWKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHOAFL 1080	
DB	1021 FHQQVWKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHOAFL 1080	
QY	1081 KLTRHRVTYVPLIGSLRTAQTLQSRKLPCTTTLTALEAAANPALPSDFKILTD 1132	
DB	1081 KLTRHRVTYVPLIGSLRTAQTLQSRKLPCTTTLTALEAAANPALPSDFKILTD 1132	
RESULT 4		
AAAY32090		
ID	AAAY32090 standard; protein; 1132 AA.	
XX		
AC	AAAY32090;	
XX		
DT	17-JAN-2000 (first entry)	
XX		
DE	Human telomerase reverse transcriptase (hTERT).	
XX		
KW	Telomerase reverse transcriptase; human; hTERT; cell proliferation; cancer.	
XX		
OS	Homo sapiens.	
XX		
PN	WO950386-A2.	
XX		
PD	07-OCT-1999.	
XX		
PF	31-MAR-1999; 99WO-US007097.	
XX		
PR	31-MAR-1998; 98US-00052864.	
PR	03-AUG-1998; 98US-00128354.	
XX		
PA	(GERO-) GERON CORP.	
XX		
PI	Morin GB;	
XX		
XX	WPI; 1999-610842/52.	
DR	N-PSDB; AA220279.	
XX		
PT	New catalytic polypeptide and polynucleotide, useful for increasing catalytic activity in a cell.	
XX		
PS	Claim 13; Fig 1; 24pp; English.	
XX		
CC	The present sequence represents human telomerase reverse transcriptase (hTERT). Human telomerase is a target for diagnosing and treating diseases relating to cell proliferation and senescence, such as cancer, or for increasing the proliferative capacity of a cell. A claimed method for increasing the proliferative capacity of a vertebrate cell, especially a human or other mammalian cell, involves introducing into the cell a recombinant hTERT polynucleotide encoding an hTERT variant in which residues 192-323, 200-323, 192-271, 200-271, 222-240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 of the present sequence are deleted. A claimed method of preparing recombinant telomerase involves contacting a recombinant hTERT deletion mutant (as above) with a telomerase RNA component such that the 2 proteins associate to form a complex capable of catalysing the addition of nucleotides to a telomerase substrate. A claimed method for reducing telomerase activity in a cell involves introducing a recombinant polynucleotide encoding an hTERT variant having a deletion of amino acids 192-450, 560-565, 637-660, 638-660, 748-764 or 1055-1071 of the present sequence	
XX		
SQ	Sequence 1132 AA;	
	Query Match 100.0%; Score 5961; DB 2; Length 1132;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MPRAPRCRAVRSLLRSHRYEVLPLATFVRRLLGQGMRLVORGDPAAAFRALVAOCLVCVPW 60	

Db 1 MPAPRCRAVSLRSHYREVLPLATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCVPW 60  
QY 61 DARPPPAAPSPROVSCLELVARVLQRLCERGAKNVLAFAFGALLDGGARGGPEAFTTSVR 120  
Db 61 DARPPPAAPSPROVSCLELVARVLQRLCERGAKNVLAFAFGALLDGGARGGPEAFTTSVR 120  
QY 121 SYLNTVTDALRGSGAGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Db 121 SYLNTVTDALRGSGAGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
QY 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGASRSRLPLPKPRR 240  
Db 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGASRSRLPLPKPRR 240  
QY 241 GAAPEPERTPVQGSWAHPGTRGSPDRGFCVSPAPAEATSLGALSGTRISHPSVG 300  
Db 241 GAAPEPERTPVQGSWAHPGTRGSPDRGFCVSPAPAEATSLGALSGTRISHPSVG 300  
QY 301 RQHAGPPSTSRPRPMDTPCPPVYAEKHFLLYSSGDKQELRPSFLJSSLRPSLTGARRL 360  
Db 301 RQHAGPPSTSRPRPMDTPCPPVYAEKHFLLYSSGDKQELRPSFLJSSLRPSLTGARRL 360  
QY 361 VETIFLGSRPMPGTPRRLPLPQRYWQMRPLFLELLGNHAQCYPGYLLKTHCPLEAAVT 420  
Db 361 VETIFLGSRPMPGTPRRLPLPQRYWQMRPLFLELLGNHAQCYPGYLLKTHCPLEAAVT 420  
QY 421 PAAGVCAREKQGSVAAPPEEDTPRRLVQLLRQHSPPWQVYGFVRACLRLRLVPPGLWGS 480  
Db 421 PAAGVCAREKQGSVAAPPEEDTPRRLVQLLRQHSPPWQVYGFVRACLRLRLVPPGLWGS 480  
QY 481 RHNERFLRNTKFTISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVCPVPAEHLREEI 540  
Db 481 RHNERFLRNTKFTISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVCPVPAEHLREEI 540  
QY 541 LAKFLHMLMSVYVELLRSPFYVTETTFQKNRLFPYKSVWSKLQSGIROHLKRVQIRE 600  
Db 541 LAKFLHMLMSVYVELLRSPFYVTETTFQKNRLFPYKSVWSKLQSGIROHLKRVQIRE 600  
QY 601 LSEAEVQHRARPALLTSRLRFTPKPDGLRPIVNDVVGARTFREKRAERTSRVKA 660  
Db 601 LSEAEVQHRARPALLTSRLRFTPKPDGLRPIVNDVVGARTFREKRAERTSRVKA 660  
QY 661 LFSVLNERARRPGLGASVLGLDDIHRAMRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720  
Db 661 LFSVLNERARRPGLGASVLGLDDIHRAMRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720  
QY 721 PODRLTEVIASIIKPNQTYCVRRAVAVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780  
Db 721 PODRLTEVIASIIKPNQTYCVRRAVAVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780  
QY 781 QETSPLRDVAVIEQSSLINEASSGLFDVFLRFMCHAVRIRGKSVYOCQIPGSGIISLTL 840  
Db 781 QETSPLRDVAVIEQSSLINEASSGLFDVFLRFMCHAVRIRGKSVYOCQIPGSGIISLTL 840  
QY 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLVLTPLHTHAKTFLRTLVRGPEYGCVVNL 900  
Db 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLVLTPLHTHAKTFLRTLVRGPEYGCVVNL 900  
QY 901 RKTVMNPFVEALGGTAFVQMPAHGLFPWCGLLDDTTLTLEVSQDSSYARTSIRASLTF 960  
Db 901 RKTVMNPFVEALGGTAFVQMPAHGLFPWCGLLDDTTLTLEVSQDSSYARTSIRASLTF 960  
QY 961 NRGFKAGNMRKLPGLVRLKCHSLFDLQVNSIQTVCTNLYKILLQAYRFHACVQLP 1020  
Db 961 NRGFKAGNMRKLPGLVRLKCHSLFDLQVNSIQTVCTNLYKILLQAYRFHACVQLP 1020  
QY 1021 FHOQWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080  
Db 1021 FHOQWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080  
QY 1081 KLTRHRTVYVPLLSGLSTAQTQLSRKLPFGTTLTALAAANPALSPDFKTILD 1132

Db 1081 KLTRHRTVYVPLLSGLSTAQTQLSRKLPFGTTLTALAAANPALSPDFKTILD 1132  
RESULT 5  
RAY43621  
ID AAY43621 standard; protein; 1132 AA.  
XX AC AAY43621;  
XX DT 26-JAN-2000 (first entry)  
XX DE A human telomerase reverse transcriptase (TRT) polypeptide.  
XX KW Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;  
XX KW dendritic cell; telomerase activity; cancer cell; proliferating cell;  
XX KW immunological destruction; telomerase; cancer; proliferation disease.  
XX OS Homo sapiens.  
XX FN WO9950392-A1.  
XX PD 07-OCT-1999.  
XX PF 30-MAR-1999; 99WO-US0006898.  
XX PR 31-MAR-1998; 98US-0112006P.  
XX PA (GERO-) GERON CORP.  
XX PI Gaeta FCA;  
XX DR WPI; 1999-610845/52.  
XX DR N-PSDB; AAZ30154.  
XX PT Eliciting an in vivo immune response for prevention and treatment of  
XX PS cancers.  
XX PS Claim 3; Fig 1; 26pp; English.  
CC The present sequence represents a human telomerase reverse transcriptase  
CC (TRT) polypeptide. The protein is used in the method of the invention.  
CC The specification describes a method for activating a T lymphocyte,  
CC comprising contacting the T lymphocyte with a dendritic cell that  
CC expresses a TRT peptide in the context of a MHC class I or MHC class II  
CC molecule. The protein causes induction of an in vivo immunological  
CC response to telomerase activity. Cancer cells are characterized by  
CC expression of endogenous TRT gene and the presence of detectable  
CC telomerase activity. Therefore, by eliciting a specific immune response  
CC to TRT or to TRT-expressing cells, it is possible to selectively target  
CC proliferating cells for immunological destruction. The method is used for  
CC eliciting an in vivo immune response to telomerase by activating a T  
CC lymphocyte, and is useful for prevention and treatment of cancers and  
CC other proliferation diseases/conditions  
XX SQ Sequence 1132 AA;  
Query Match 100.0%; Score 5961; DB 2; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPAPRCRAVSLRSHYREVLPLATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCVPW 60  
Db 1 MPAPRCRAVSLRSHYREVLPLATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCVPW 60  
QY 61 DARPPPAAPSPROVSCLELVARVLQRLCERGAKNVLAFAFGALLDGGARGGPEAFTTSVR 120  
Db 61 DARPPPAAPSPROVSCLELVARVLQRLCERGAKNVLAFAFGALLDGGARGGPEAFTTSVR 120  
QY 121 SYLNTVTDALRGSGAGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Db 121 SYLNTVTDALRGSGAGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
QY 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGASRSRLPLPKPRR 240

Db 181 ATQARPPHAGRRRRIGCCRAMNHSVREAGVPLGLPAPGARRGGSSASRLPLPKRPR 240  
Qy 241 GAAPERTPTVGGQSWAHGRTGSDRGFCVWSPARPAEATSLGALSCTRHSHPSVG 300  
Db 241 GAAPERTPTVGGQSWAHGRTGSDRGFCVWSPARPAEATSLGALSCTRHSHPSVG 300  
Qy 301 RQHAGPPSTSRPPRWDTPCPVYAEKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360  
Db 301 RQHAGPPSTSRPPRWDTPCPVYAEKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360  
Qy 361 VETIFLGSRRPMCTPRRLPRLPQRYWQMRPLFLELLGNHAOCYPGVLLKTHCPLRAAVT 420  
Db 361 VETIFLGSRRPMCTPRRLPRLPQRYWQMRPLFLELLGNHAOCYPGVLLKTHCPLRAAVT 420  
Qy 421 PAAGVCAREKPOGSVAAPPEEDTPRRLVOLLQHSPPWQVYFVRACLRRLVPPGLWGS 480  
Db 421 PAAGVCAREKPOGSVAAPPEEDTPRRLVOLLQHSPPWQVYFVRACLRRLVPPGLWGS 480  
Qy 481 RHNERFLRNTKXIFSLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540  
Db 481 RHNERFLRNTKXIFSLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540  
Qy 541 LAKFLHWMVYVVELLSRFYVTTTFQKNRLFYRKSVWSKLSQSIGIRQHLYKRVOLRE 600  
Db 541 LAKFLHWMVYVVELLSRFYVTTTFQKNRLFYRKSVWSKLSQSIGIRQHLYKRVOLRE 600  
Qy 601 LSAEVRQREARPAALLTSRLRIPKPDGLRPIVNDYVVGATFERREKBAELTSRVKA 660  
Db 601 LSAEVRQREARPAALLTSRLRIPKPDGLRPIVNDYVVGATFERREKBAELTSRVKA 660  
Qy 661 LFSVLNTERARRPCLLGASVLGDDIHRAWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720  
Db 661 LFSVLNTERARRPCLLGASVLGDDIHRAWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720  
Qy 721 PQRLTEVIASIIKPQNTYCVRYAVVQKAAHGHVKAFFKSHVSTLTDLPYMRQFVAHL 780  
Db 721 PQRLTEVIASIIKPQNTYCVRYAVVQKAAHGHVKAFFKSHVSTLTDLPYMRQFVAHL 780  
Qy 781 QETSPLRDAVVIQSSSLNEASGLFDVFLRFMCHHAVIRGKSYVQCQIPGSSILSTL 840  
Db 781 QETSPLRDAVVIQSSSLNEASGLFDVFLRFMCHHAVIRGKSYVQCQIPGSSILSTL 840  
Qy 841 LCSLCYGD MENKLFAGIRRDGLLRLVDLFLVTPHLTHAKTFLRTLVRGVPEYGCVNIL 900  
Db 841 LCSLCYGD MENKLFAGIRRDGLLRLVDLFLVTPHLTHAKTFLRTLVRGVPEYGCVNIL 900  
Qy 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSSYARTSIRASLTF 960  
Db 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSSYARTSIRASLTF 960  
Qy 961 NRGFKAGRNRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRRHACVLQLP 1020  
Db 961 NRGFKAGRNRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRRHACVLQLP 1020  
Qy 1021 FHQVQWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWLCHQAFLL 1080  
Db 1021 FHQVQWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWLCHQAFLL 1080  
Qy 1081 KLTRHRVTVYVPLGLSRLTAQTQLSRKLPGTTLTALEAANPALPSDFKTLTD 1132  
Db 1081 KLTRHRVTVYVPLGLSRLTAQTQLSRKLPGTTLTALEAANPALPSDFKTLTD 1132

RESULT 6  
AAV26580  
ID AAY26580 standard; protein; 1132 AA.  
XX  
AC AAY26580;  
XX  
DT 13-SEP-1999 (first entry)  
XX  
DE Human telomerase reverse transcriptase (hTERT) enzyme.

XX  
KW Telomerase reverse transcriptase; TERT; mouse; telomere length assay;  
KW immunogen; enzyme; telomerase-mediated DNA replication; human.  
OS Homo sapiens.  
XX  
FN WO9927113-A1.  
XX  
PD 03-JUN-1999.  
XX  
PF 25-NOV-1998; 98WO-US025211.  
XX  
PR 26-NOV-1997; 97US-00979742.  
PR 16-MAR-1998; 98US-00042460.  
XX  
(GERO-) GERON CORP.  
PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.  
XX  
PI Morin GB, Allsopp R, Depinho R, Greenberg R;  
XX WPI; 1999-347722/29.  
XX  
PT Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and  
PT nucleic acids.  
XX  
PS Disclosure; Fig 3; 135pp; English.  
XX  
CC The invention relates to a mouse telomerase reverse transcriptase (mTERT)  
CC enzyme. Compositions containing mTERT can be used in telomere length  
CC assays. Isolated mTERT is useful as an immunogen for the production of  
CC monoclonal or polyclonal antibodies. The method is useful for assessing  
CC the degree of purification and identification of new mTERT species, such  
CC as an mTERT allele, homolog or isoform, or to screen for modulators  
CC (antagonists and agonists) of telomerase-mediated DNA replication.  
CC Antagonists and agonists of mTERT can be used to modify the activity of  
CC other telomerase enzymes such as human TERT (hTERT). The present sequence  
CC represents a human TERT enzyme  
XX  
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;  
Best Local Similarity 100.0%; Fred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRAPRCRAVRSLRSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCVPW 60  
Db 1 MPRAPRCRAVRSLRSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCVPW 60  
Qy 61 DARPPAAPSPFQVSCLEKELVARVQLRCLERCAGKNVLAFFGALLDGARGGPEAFTTSVR 120  
Db 61 DARPPAAPSPFQVSCLEKELVARVQLRCLERCAGKNVLAFFGALLDGARGGPEAFTTSVR 120  
Qy 121 SYLPTNTVDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Db 121 SYLPTNTVDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Qy 181 ATQAQAPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGSSASRLPLPKRPRR 240  
Db 181 ATQAQAPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGSSASRLPLPKRPRR 240  
Qy 241 GAAPERTPTVGGQSWAHGRTGSDRGFCVWSPARPAEATSLGALSCTRHSHPSVG 300  
Db 241 GAAPERTPTVGGQSWAHGRTGSDRGFCVWSPARPAEATSLGALSCTRHSHPSVG 300  
Qy 301 ROHAGPPSTSRPPRWDTPCPVYAEKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360  
Db 301 ROHAGPPSTSRPPRWDTPCPVYAEKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360  
Qy 361 VETIFLGSRRPMCTPRRLPRLPQRYWQMRPLFLELLGNHAOCYPGVLLKTHCPLRAAVT 420  
Db 361 VETIFLGSRRPMCTPRRLPRLPQRYWQMRPLFLELLGNHAOCYPGVLLKTHCPLRAAVT 420  
Qy 421 PAAGVCAREKPOGSVAAPPEEDTPRRLVOLLQHSPPWQVYFVRACLRRLVPPGLWGS 480

Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSFPWQYGVFVRACLRRLVPPGLWGS 480  
Qy 481 RHNERRFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540  
Db 481 RHNERRFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540  
Qy 541 LAKFLHLMMSVYVVELLRSFFYVTTTFOKNRLFYFYSKSVMSKLSQSIGIRQHLKRVQRE 600  
Db 541 LAKFLHLMMSVYVVELLRSFFYVTTTFOKNRLFYFYSKSVMSKLSQSIGIRQHLKRVQRE 600  
Qy 601 LSEAEVQHREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660  
Db 601 LSEAEVQHREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660  
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELVFKVDVGTAYDTI 720  
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELVFKVDVGTAYDTI 720  
Qy 721 PQDLRTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780  
Db 721 PQDLRTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780  
Qy 781 QETSPLRDADVIEOSSSNEASSGLFDVFLRPMCHHAVIRGKSYVQCGIPIQGSII STL 840  
Db 781 QETSPLRDADVIEOSSSNEASSGLFDVFLRPMCHHAVIRGKSYVQCGIPIQGSII STL 840  
Qy 841 LCSLCYGMENKLFAGTRRDDGLLRLVDDFLVTPHLLTHAKTFURTLVIRGVPEYGCVVNL 900  
Db 841 LCSLCYGMENKLFAGTRRDDGLLRLVDDFLVTPHLLTHAKTFURTLVIRGVPEYGCVVNL 900  
Qy 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVSQSDYSYARTSIRASLTF 960  
Db 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVSQSDYSYARTSIRASLTF 960  
Qy 961 NRGFKAGNRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLLOAQRHFACVLQLP 1020  
Db 961 NRGFKAGNRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLLOAQRHFACVLQLP 1020  
Qy 1021 FHOQVKNPFFLRFVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHOAFL 1080  
Db 1021 FHOQVKNPFFLRFVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHOAFL 1080  
Qy 1081 KLTRHRTYVPLGLSLRTAQQLSRKLPFGTTLTALEAAANPALPSDFKTI 1132  
Db 1081 KLTRHRTYVPLGLSLRTAQQLSRKLPFGTTLTALEAAANPALPSDFKTI 1132

RESULT 7

AAG64859  
ID AAG64859 standard; protein; 1132 AA.  
XX AC AAG64859;  
XX AC AAG64859;  
DT 21-SEP-2001 (first entry)  
DE Heart muscle cell differentiation related protein SEQ ID NO: 31.  
XX KW Heart muscle cell; human; cell differentiation; heart disease.  
XX OS Homo sapiens.  
XX PN W0200148151-A1.  
XX PD 05-JUL-2001.  
XX PF 27-DEC-2000; 2000WO-JP009323.  
XX PR 28-DEC-1999; 99JP-00372826.  
XX PR 28-FEB-2000; 2000WO-JP001148.  
XX PR 02-NOV-2000; 2000WO-JP007741.  
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;  
PI Yamada Y;  
XX WPI; 2001-425656/45.  
DR N-PSDB; AAH48235.  
XX Cells capable of differentiating into cardiomyocytes and originating in  
PT bone marrow or umbilical blood cells for study of cardiomyocyte  
PT differentiation and treatment of heart disease.  
XX  
PS Claim 87; Page 143-147; 183pp; Japanese.  
XX  
CC The present invention provides cells originating in the human bone marrow  
CC or umbilical blood cells which are capable of differentiating into  
CC cardiomyocytes. These cells are useful in the treatment of diseases  
CC involving heart muscle degeneration, such as myocardial infarction, and  
CC the study of cardiomyocyte differentiation. The present sequence is a  
CC protein described in the exemplification of the invention  
XX  
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGQWRLVORGPAAFRALVAOCLVCVPW 60  
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGQWRLVORGPAAFRALVAOCLVCVPW 60  
Qy 61 DARPPPAAPFRQVSCLELVARVQLRCERGAANVLAFGALLDARGGPPPEAFTTSVR 120  
Db 61 DARPPPAAPFRQVSCLELVARVQLRCERGAANVLAFGALLDARGGPPPEAFTTSVR 120  
Qy 121 SYLPTVTDALRSGGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYVCGPPLYQLGA 180  
Db 121 SYLPTVTDALRSGGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYVCGPPLYQLGA 180  
Qy 181 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAGCARRRGGSASRLPLPKPRR 240  
Db 181 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAGCARRRGGSASRLPLPKPRR 240  
Qy 241 GAAPEPERTPVGGQSWAHPCGTRGSDRGFCVVSAPARPAEEATSEALSGTRHSHPSVG 300  
Db 241 GAAPEPERTPVGGQSWAHPCGTRGSDRGFCVVSAPARPAEEATSEALSGTRHSHPSVG 300  
Qy 301 RQHAGPPSTSRPRPMDTPCPVYATKHFLYSSGDKQELRPSFLLSLRPSLTGARRL 360  
Db 301 RQHAGPPSTSRPRPMDTPCPVYATKHFLYSSGDKQELRPSFLLSLRPSLTGARRL 360  
Qy 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMPLELLELGNHAQCPYGVLLKTHCPLRAVT 420  
Db 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMPLELLELGNHAQCPYGVLLKTHCPLRAVT 420  
Qy 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSFPWQYGVFVRACLRRLVPPGLWGS 480  
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSFPWQYGVFVRACLRRLVPPGLWGS 480  
Qy 481 RHNERRFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540  
Db 481 RHNERRFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540  
Qy 541 LAKFLHLMMSVYVVELLRSFFYVTTTFOKNRLFYFYSKSVMSKLSQSIGIRQHLKRVQRE 600  
Db 541 LAKFLHLMMSVYVVELLRSFFYVTTTFOKNRLFYFYSKSVMSKLSQSIGIRQHLKRVQRE 600  
Qy 601 LSEAEVQHREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660  
Db 601 LSEAEVQHREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660  
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELVFKVDVGTAYDTI 720  
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELVFKVDVGTAYDTI 720

QY 721 PODRLTEVIASIIKQNTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780  
DB 721 PODRLTEVIASIIKQNTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780  
QY 781 QETSPLRDAVVEIQSSSINEASSGLFVFLRFMCHHAVRIRGKSVQCOGIPQGSII STL 840  
DB 781 QETSPLRDAVVEIQSSSINEASSGLFVFLRFMCHHAVRIRGKSVQCOGIPQGSII STL 840  
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900  
DB 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900  
QY 901 RKTVVNFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDSYARTSIRASLTIF 960  
DB 901 RKTVVNFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDSYARTSIRASLTIF 960  
QY 961 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020  
DB 961 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020  
QY 1021 FHOQWKNPTEFLRVIDSTASLCYSILKAKVAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080  
DB 1021 FHOQWKNPTEFLRVIDSTASLCYSILKAKVAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080  
QY 1081 KLTRHRVTVYVPLGLSLRTAQTLGRKLPGLTTLTALEAAANPALPSPDFKTILD 1132  
DB 1081 KLTRHRVTVYVPLGLSLRTAQTLGRKLPGLTTLTALEAAANPALPSPDFKTILD 1132

## RESULT 8

AAG64329  
ID AAG64329 standard; protein; 1132 AA.  
AC AAG64329;  
XX  
DT 24-SEP-2001 (first entry)  
XX  
XX Human protein #2.  
XX Angiogenesis; cardiatic; cell differentiating agent; bone marrow;  
XX heart muscle cell; heart disease; human.  
XX Homo sapiens.  
XX WO200148149-A1.  
XX  
XX 05-JUL-2001.  
XX  
XX 28-FEB-2000; 2000WO-JP001148.  
XX  
XX 28-DEC-1999; 99JP-00372826.  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K;  
XX  
XX WPI; 2001-418252/44.  
XX N-PSDB; AAH49601.  
XX  
XX New adult bone marrow-originated cells capable of differentiating into  
XX heart muscle cells, applicable as remedies for various heart diseases  
XX particularly with damaged heart muscle accompanying degeneration.  
XX  
XX Disclosure; Page 128-134; 158pp; Japanese.  
XX  
XX The present invention relates to cells isolated from bone marrow, which  
XX are capable of at least differentiating into heart muscle cells. The  
XX cells are applicable as remedies for various heart diseases particularly  
XX with damaged heart muscle accompanying degeneration. The present sequence  
XX was used to illustrate the present invention  
XX  
XX Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPAPPCRAVRSLLRSHYREVLPATFVRRLGQGWRLVQRGDPAAFRALVAOCLVCVPW 60  
DB 1 MPAPPCRAVRSLLRSHYREVLPATFVRRLGQGWRLVQRGDPAAFRALVAOCLVCVPW 60  
QY 61 DARPPPAASFRQVSCLELVARVLRQRCERAGKNVLAFGFALLDGCARGGPPPEAFTTSVR 120  
DB 61 DARPPPAASFRQVSCLELVARVLRQRCERAGKNVLAFGFALLDGCARGGPPPEAFTTSVR 120  
QY 121 SYLNTVTDALRGSGAWGLLLRRVDDVLVHLLARCALEVLVAPSCAYQVCGPPLYQLGA 180  
DB 121 SYLNTVTDALRGSGAWGLLLRRVDDVLVHLLARCALEVLVAPSCAYQVCGPPLYQLGA 180  
QY 181 ATQARPPPHASGPRRLGGERAWNHSVRAGVPLGLPAPGARRRGGSAGRSPLPKRPRR 240  
DB 181 ATQARPPPHASGPRRLGGERAWNHSVRAGVPLGLPAPGARRRGGSAGRSPLPKRPRR 240  
QY 241 GAAPPERTPVQGGSWAHFPGTRGSDRGFCVVSAPPAEATSLGALSGRTRHSHPSVG 300  
DB 241 GAAPPERTPVQGGSWAHFPGTRGSDRGFCVVSAPPAEATSLGALSGRTRHSHPSVG 300  
QY 301 ROHAGPPSTSRPPRWDTPCPVYAETHKFLYSSGDKBQLRPSFLLSLRPSLTGARL 360  
DB 301 ROHAGPPSTSRPPRWDTPCPVYAETHKFLYSSGDKBQLRPSFLLSLRPSLTGARL 360  
QY 361 VETIFLGRSPWMPGTPRRLPRLPQRYWQMRPLFELGNHACQPGVLLKTHCPRAAVT 420  
DB 361 VETIFLGRSPWMPGTPRRLPRLPQRYWQMRPLFELGNHACQPGVLLKTHCPRAAVT 420  
QY 421 PAAGVCAREKPOGSVAAPPEEDTDPRRLVQLLRQHSSPWQYVGFVRACLRLRVPGLWGS 480  
DB 421 PAAGVCAREKPOGSVAAPPEEDTDPRRLVQLLRQHSSPWQYVGFVRACLRLRVPGLWGS 480  
QY 481 RHNERFLRNTKFFISLGHAKLSLOBLTWKMSVRDCAWLRRSPGCVGCPAAEHLRBEI 540  
DB 481 RHNERFLRNTKFFISLGHAKLSLOBLTWKMSVRDCAWLRRSPGCVGCPAAEHLRBEI 540  
QY 541 LAKFLHLMWSVYVVELLSRFFVTTTFOKRLFPYRSVMSKLSIGIRHOLKRVQURE 600  
DB 541 LAKFLHLMWSVYVVELLSRFFVTTTFOKRLFPYRSVMSKLSIGIRHOLKRVQURE 600  
QY 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRKA 660  
DB 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRKA 660  
QY 661 LFSVLNARARPPGLLGASVLGLDDIHRAWTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720  
DB 661 LFSVLNARARPPGLLGASVLGLDDIHRAWTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720  
QY 721 PQDRLTEVIASIIKQNTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780  
DB 721 PQDRLTEVIASIIKQNTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780  
QY 781 QETSPLRDAVVEIQSSSINEASSGLFVFLRFMCHHAVRIRGKSVQCOGIPQGSII STL 840  
DB 781 QETSPLRDAVVEIQSSSINEASSGLFVFLRFMCHHAVRIRGKSVQCOGIPQGSII STL 840  
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900  
DB 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900  
QY 901 RKTVVNFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDSYARTSIRASLTIF 960  
DB 901 RKTVVNFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDSYARTSIRASLTIF 960  
QY 961 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020  
DB 961 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020



Qy 1021 FHOQWKNPFFLRVISDTSALCYSLKAKNAGMSLGAKGAGDPLPSEAVOWLCHQAFLL 1080  
Db 1021 FHOQWKNPFFLRVISDTSALCYSLKAKNAGMSLGAKGAGDPLPSEAVOWLCHQAFLL 1080  
Qy 1081 KLTRHRVTYVPLLSGLRTAQQLSRKLPQTTLTALAAANPALPSDFKTILD 1132  
Db 1081 KLTRHRVTYVPLLSGLRTAQQLSRKLPQTTLTALAAANPALPSDFKTILD 1132

RESULT 9

AAB99930  
ID AAB99930 standard; protein; 1132 AA.  
XX AAB99930;  
AC AAB99930;  
XX  
DT 26-SEP-2001 (first entry)  
XX Human telomerase protein sequence SEQ ID NO:31.  
DE  
XX  
KW Differentiation; heart muscle cell; cytokine; transcription factor;  
KW proliferation; surface antigen; heart disease; cardiomyocyte;  
KW bone marrow; umbilical blood cell; heart muscle degeneration;  
KW myocardial infarction.  
XX  
OS Homo sapiens.  
XX WO200148150-A1.  
XX  
PD 05-JUL-2001.  
XX  
PF 02-NOV-2000; 2000WO-JP007741.  
XX  
PR 28-DEC-1999; 99JP-00372826.  
PR 28-FEB-2000; 2000WO-JP001148.  
XX  
XX (KTOW ) KYOWA HAKKO KOGYO KK.  
PA  
XX  
XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;  
PI Yamada Y;  
XX  
DR WPI; 2001-425655/45.  
DR N-FSDB; AAH44366.  
XX

Cells capable of differentiating into cardiomyocytes and originating in bone marrow or umbilical blood cells for study of cardiomyocyte differentiation and treatment of heart disease.

Claim 146; Page 137-141; 187pp; Japanese.

The present invention describes cells originating in bone marrow or umbilical blood cells which are capable of differentiating into cardiomyocytes. Also described are: (1) cardiomyocytes produced by the differentiation of the cells; (2) a method for carrying out the differentiation into cardiomyocytes, regulated by a promotional and/or inhibitory factor; (3) a method for the differentiation of the cells into cell types other than cardiomyocytes; (4) drug compositions promoting the formation of heart muscle and regeneration of heart tissue which contain the cells; (5) a method for the production of antibodies which recognise the cells, especially antibodies which recognise a surface antigen on the cells; (6) a method for screening factors which promote the proliferation of the cells; (7) a method for immortalising the cells by expressing telomerase in them; (8) drug compositions for the treatment of heart disease which contain the immortalised cells; and (9) cell-free supernatant from the culture of the cells and its use in promoting their differentiation into cardiomyocytes. The cells are used in the treatment of diseases involving heart muscle degeneration, such as myocardial infarction and in the study of cardiomyocyte differentiation. AAH44351 to AAH44409 and AAB99915 to AAB99935 represent sequences used in the exemplification of the present invention

Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLPGQWMLVQRGDPAAPRALVAOCLVCVPW 60  
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLPGQWMLVQRGDPAAPRALVAOCLVCVPW 60  
Qy 61 DAPPPAAPSFQVSCIKELVARVLQRLCERGANVLAFGFALLDARGGPEAFTTSVR 120  
Db 61 DAPPPAAPSFQVSCIKELVARVLQRLCERGANVLAFGFALLDARGGPEAFTTSVR 120  
Qy 121 SYLPNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180  
Db 121 SYLPNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180  
Qy 181 ATQARPPPHASGPRRRLGCERANNHVSREAGVPLGLPAPGARRRGGSASRSLPLPKPRR 240  
Db 181 ATQARPPPHASGPRRRLGCERANNHVSREAGVPLGLPAPGARRRGGSASRSLPLPKPRR 240  
Qy 241 GAAPERTPVGGQSWAHPOGTRGSPDRGFCVSPARPABEATSLEGALSGTRHSHPSVG 300  
Db 241 GAAPERTPVGGQSWAHPOGTRGSPDRGFCVSPARPABEATSLEGALSGTRHSHPSVG 300  
Qy 301 ROHHAGPPSTSRPPRWDTPCPVPVYAEKHFLYSSGDKQLRPSFLSLRPSLTGARRL 360  
Db 301 ROHHAGPPSTSRPPRWDTPCPVPVYAEKHFLYSSGDKQLRPSFLSLRPSLTGARRL 360  
Qy 361 VETIFLGSRPWMPGTPELRLPRLPORVWQMRPLFLELGNHAQCPYGVLLKTHCPLEAAVT 420  
Db 361 VETIFLGSRPWMPGTPELRLPRLPORVWQMRPLFLELGNHAQCPYGVLLKTHCPLEAAVT 420  
Qy 421 PAAGVCAREKPOGSAVAPEEEDTPRELVLQRLRHSSFPWQYGFVRACLRRLVPPGLWGS 480  
Db 421 PAAGVCAREKPOGSAVAPEEEDTPRELVLQRLRHSSFPWQYGFVRACLRRLVPPGLWGS 480  
Qy 481 RHNERFLRNTKFIISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLBEI 540  
Db 481 RHNERFLRNTKFIISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLBEI 540  
Qy 541 LAKFLHMLMSVYVVELLRSFFYVTTTFQKNRFFYRKSVMKLSQSIGRHLKRVOLRE 600  
Db 541 LAKFLHMLMSVYVVELLRSFFYVTTTFQKNRFFYRKSVMKLSQSIGRHLKRVOLRE 600  
Qy 601 LSEAEVRQHREARPAALTSRLRPIKPDGLRPVNMMDYVVGARTFREKRAERLTSRKA 660  
Db 601 LSEAEVRQHREARPAALTSRLRPIKPDGLRPVNMMDYVVGARTFREKRAERLTSRKA 660  
Qy 661 LFSVLNYERARRPGLLGASVGLDLDIHRWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720  
Db 661 LFSVLNYERARRPGLLGASVGLDLDIHRWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720  
Qy 721 POBELTEVIASIIKPNQTYCVRRYAVYVQAAHGHVKAFFKSHVSTLTLQPYMFOFVAHL 780  
Db 721 POBELTEVIASIIKPNQTYCVRRYAVYVQAAHGHVKAFFKSHVSTLTLQPYMFOFVAHL 780  
Qy 781 QETSPLRDADVIVQSSSLNEASGLFDVFLRFMCHHAVIRGKSYVOCQIGIPQGSILSTL 840  
Db 781 QETSPLRDADVIVQSSSLNEASGLFDVFLRFMCHHAVIRGKSYVOCQIGIPQGSILSTL 840  
Qy 841 LCSLCYGDMMENKLFAGIRRDGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEPYGCVVNL 900  
Db 841 LCSLCYGDMMENKLFAGIRRDGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEPYGCVVNL 900  
Qy 901 RKTVMNPFVDEALGGTAFVOMPAHGLFPWCGLLDTRTLEQSDYSYARTSIRASLTFF 960  
Db 901 RKTVMNPFVDEALGGTAFVOMPAHGLFPWCGLLDTRTLEQSDYSYARTSIRASLTFF 960  
Qy 961 NRGFKAGNNRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020  
Db 961 NRGFKAGNNRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020  
Qy 1021 FHOQWKNPFFLRVISDTSALCYSLKAKNAGMSLGAKGAGDPLPSEAVOWLCHQAFLL 1080

Db 1021 FHQOVKNPTFFLRVISTASLCVSLKAKNAGKMSLGAKGAAGLPSEAVQWICHOAFLL 1080  
Qy 1081 KLTRHRVYVPLGSLRTAQQLSRKLPGLTTLTALEAANPALPSPDKTILD 1132  
|||||  
Db 1081 KLTRHRVYVPLGSLRTAQQLSRKLPGLTTLTALEAANPALPSPDKTILD 1132

RESULT 10  
AAB82765  
ID AAB82765 standard; protein; 1132 AA.  
XX  
AC AAB82765;  
XX  
DT 29-OCT-2001 (first entry)  
XX  
DE Human telomerase reverse transcriptase.  
XX  
KW Telomerase reverse transcriptase; hTERT; human; cancer; tumour;  
KW cytotoxic T lymphocyte; major histocompatibility complex;  
KW human leucocyte antigen; HLA-A2.1; vaccine.  
XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT Peptide 13..21  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 23..31  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 76..84  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 96..104  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 140..148  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 152..160  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 346..354  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 353..361  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 371..379  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 388..396  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 407..415  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 487..495  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 540..548  
FT /label= p540  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 548..556  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 555..563  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 572..580  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 705..713  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 724..732  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 772..780  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 797..805  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 812..820  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 836..844  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 863..871  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 865..873  
FT /label= p865

FT Peptide /note= "HLA-A2.1 binding motif"  
FT 883..891  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 926..934  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 934..942  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 969..977  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 988..996  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 1072..1080  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 1079..1087  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 1095..1103  
FT /note= "HLA-A2.1 binding motif"  
FT Peptide 1122..1130  
FT /note= "HLA-A2.1 binding motif"  
XX  
XX WO200160391-A1.  
XX  
XX 23-AUG-2001.  
XX  
XX 15-FEB-2001; 2001WO-US005143.  
XX  
PR 15-FEB-2000; 2000US-0182685P.  
PR 15-FEB-2001; 2001US-00182685.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Zanetti M;  
XX  
XX WPI; 2001-536552/59.  
XX  
XX Vaccine for initiating and enhancing a cytotoxic T lymphocyte response,  
FT for treating cancers or tumors or for inducing immune response against  
FT tumors, comprises a telomerase reverse transcriptase peptide.  
XX  
XX Disclosure; Fig 5; 52pp; English.  
XX  
XX The present sequence is that of human telomerase reverse transcriptase  
CC (hTERT). The sequence was analysed for 9-mer peptide sequences containing  
CC known binding motifs for the human leukocyte antigen HLA-A2.1 molecule.  
CC From an initial panel of about 30 candidate peptides, 2 sequences,  
CC denoted p540 (see AAB82772) and p865 (see AAB82773), were examined. The  
CC majority of healthy individuals as well as patients with prostate cancer  
CC immunised in vitro against these 2 HLA-A2.1 restricted peptides developed  
CC hTERT-specific cytotoxic T lymphocytes (CTL). The cancer patients' CTL  
CC specifically lysed a variety of HLA-A2+ cancer cell lines such as  
CC prostate, breast, colon, lung and melanoma, demonstrating immunological  
CC recognition of endogenously-processed hTERT peptides. In vivo immunisation  
CC of HLA-A2.1 transgenic mice generated a specific CTL response against  
CC both hTERT peptides. The induction of CTL responses in vitro and in vivo,  
CC and the susceptibility to lysis of tumour cells of various origins by  
CC hTERT CTL suggest that hTERT could serve as a universal cancer vaccine for  
CC humans. Thus, a claimed universal vaccine for treating tumours of any  
CC origin comprises at least 1 hTERT peptide in an amount effective for  
CC initiating and enhancing a CTL response against cancer cells. The peptide  
CC is 7-15 amino acid residues in length and may be modified to enhance  
CC binding to the major histocompatibility complex. Also claimed is a method  
CC for inducing and enhancing a CTL response against cancer cells, involving  
CC harvesting blood leucocytes, pulsing with hTERT, and contacting cancer  
CC cells with the pulsed leucocytes. A method for targeting CTL to tumour  
CC cells is also claimed, and involves administering a hTERT peptide to a  
CC mammal, especially a cancer patient  
XX  
SQ Sequence 1132 AA;  
Query Match 100.0%; Score 5961; DB 4; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRIRLPGQWRLVORGDDPAAFRALVAQCLVCVPW 60  
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRIRLPGQWRLVORGDDPAAFRALVAQCLVCVPW 60  
Qy 61 DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVR 120  
Db 61 DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVR 120  
Qy 121 SYLPTNTVDALRSGGAWGLLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Db 121 SYLPTNTVDALRSGGAWGLLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Qy 181 ATQARPPPHASGPRRRRRCERAMNHSVREAGVPLGLPAGARRRGGSGASRSLPLPKPRR 240  
Db 181 ATQARPPPHASGPRRRRRCERAMNHSVREAGVPLGLPAGARRRGGSGASRSLPLPKPRR 240  
Qy 241 GAAPERTPTVQGSWAHPGTRGSDRGFCVSPARPAEATSILEGALSGTRSHPSVG 300  
Db 241 GAAPERTPTVQGSWAHPGTRGSDRGFCVSPARPAEATSILEGALSGTRSHPSVG 300  
Qy 301 RQHAGPSTSRPRPMDTPCPPVYAEKHFYSSGDKQELRPSFLLSLSPSLTGARRL 360  
Db 301 RQHAGPSTSRPRPMDTPCPPVYAEKHFYSSGDKQELRPSFLLSLSPSLTGARRL 360  
Qy 361 VETIFLGSRRPMPGTTPRLPLRPQYQMRPLFLELLGNHAQCYPYVLLKTHCPLRAAVT 420  
Db 361 VETIFLGSRRPMPGTTPRLPLRPQYQMRPLFLELLGNHAQCYPYVLLKTHCPLRAAVT 420  
Qy 421 PAAGVCAREKQGSVAAPPEEDTPRLVOLLROHSSPWQYVFRACLRLRVPGLWGS 480  
Db 421 PAAGVCAREKQGSVAAPPEEDTPRLVOLLROHSSPWQYVFRACLRLRVPGLWGS 480  
Qy 481 RHNERRFLRNTKFIISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540  
Db 481 RHNERRFLRNTKFIISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540  
Qy 541 LAKFLHLMMSVYVVELLRSFFYVTTTFQKNRPFYRKSVMSKLQSIGIRQHLKRVQLRE 600  
Db 541 LAKFLHLMMSVYVVELLRSFFYVTTTFQKNRPFYRKSVMSKLQSIGIRQHLKRVQLRE 600  
Qy 601 LSEAEVQHRARPAALLTSRLRFIPKPDGLRPIVNDYVVCARTFREKRAERLTSRKA 660  
Db 601 LSEAEVQHRARPAALLTSRLRFIPKPDGLRPIVNDYVVCARTFREKRAERLTSRKA 660  
Qy 661 LFSVLNTERAARRPGLGASVLGDDIHRAWTFVLVRAQDPPPELVFKVDVGTGAYDTI 720  
Db 661 LFSVLNTERAARRPGLGASVLGDDIHRAWTFVLVRAQDPPPELVFKVDVGTGAYDTI 720  
Qy 721 PODRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780  
Db 721 PODRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780  
Qy 781 QETSPLRDVAVIEOSSLINEASSGLFDVFLRPMCHHAVRIRGKSYVOCQGIPOQSII STL 840  
Db 781 QETSPLRDVAVIEOSSLINEASSGLFDVFLRPMCHHAVRIRGKSYVOCQGIPOQSII STL 840  
Qy 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVLTPLTHAKTEFLTRTVRGVPEYGCVVNL 900  
Db 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVLTPLTHAKTEFLTRTVRGVPEYGCVVNL 900  
Qy 901 RKTVVNPFVEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQDYSYARTSIRASITF 960  
Db 901 RKTVVNPFVEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQDYSYARTSIRASITF 960  
Qy 961 NRGFKAGRMNRKLFGLVLRKCHSLFLDLQVNSIQTVCTNIYKILLQAVRFHACVLOLP 1020  
Db 961 NRGFKAGRMNRKLFGLVLRKCHSLFLDLQVNSIQTVCTNIYKILLQAVRFHACVLOLP 1020  
Qy 1021 PHQVQKNPTFFLAVISDTASLCYSILKAKNAGSLGKAGAGPLPSEAVQWLCHQAFLL 1080  
Db 1021 PHQVQKNPTFFLAVISDTASLCYSILKAKNAGSLGKAGAGPLPSEAVQWLCHQAFLL 1080  
Qy 1081 KLTRHRTVYVPLGLSLRTAQQLSRKLP GTTTLTAAEAAANPALPSDFKTILD 1132

Db 1081 KLTRHRTVYVPLGLSLRTAQQLSRKLP GTTTLTAAEAAANPALPSDFKTILD 1132  
RESULT 11  
AAE29226  
ID AAE29226 standard; protein; 1132 AA.  
XX AC AAE29226;  
XX AC (first entry)  
DT 27-JAN-2003  
XX Human telomerase reverse transcriptase (TERT).  
DE Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1.3GT; TERT;  
KW transgenic; alpha(1,2)fucosyltransferase; alpha1.2FT; human; enzyme;  
KW telomerase reverse transcriptase.  
XX OS Homo sapiens.  
XX WO200274948-A2.  
XX PN 26-SEP-2002.  
XX PD  
XX 21-MAR-2002; 2002WO-CA000378.  
XX PF  
XX 21-MAR-2001; 2001US-0277811P.  
XX PR  
XX (GERO-) GERON CORP.  
XX PA Denning C, Clark AJ, Schiff JM;  
XX PI  
XX WPI: 2002-759895/82.  
XX N-PSDB: AAD46821.  
XX PT Mammalian cells, useful for producing animal tissues with carbohydrate  
antigens that are compatible for transplantation into human patients.  
XX PS Disclosure; Page 34; 71pp; English.  
XX CC The invention relates to animal tissues with carbohydrate antigens that  
are compatible for transplantation into human patients. The mammalian  
cell is inactivated homozygously for expression of alpha(1,3)galactosyl-  
transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-  
fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue  
with carbohydrate antigens that are compatible for transplantation into  
human patients. The present sequence is human telomerase reverse  
transcriptase (TERT) used in the invention  
SQ Sequence 1132 AA;  
Query Match 100.0%; Score 5961; DB 5; Length 1132;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRIRLPGQWRLVORGDDPAAFRALVAQCLVCVPW 60  
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRIRLPGQWRLVORGDDPAAFRALVAQCLVCVPW 60  
Qy 61 DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVR 120  
Db 61 DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVR 120  
Qy 121 SYLPTNTVDALRSGGAWGLLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Db 121 SYLPTNTVDALRSGGAWGLLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Qy 181 ATQARPPPHASGPRRRRRCERAMNHSVREAGVPLGLPAGARRRGGSGASRSLPLPKPRR 240  
Db 181 ATQARPPPHASGPRRRRRCERAMNHSVREAGVPLGLPAGARRRGGSGASRSLPLPKPRR 240  
Qy 241 GAAPERTPTVQGSWAHPGTRGSDRGFCVSPARPAEATSILEGALSGTRSHPSVG 300  
Db 241 GAAPERTPTVQGSWAHPGTRGSDRGFCVSPARPAEATSILEGALSGTRSHPSVG 300



Db 361 VETIFLGRSPPMPTGTPRRLLPQRYWQMRPLFLELLGNHAQCYPYGVLLKTHCPLRAAVT 420  
Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSPPQWYGFVRACLRLRLVPPGLWGS 480  
Db 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSPPQWYGFVRACLRLRLVPPGLWGS 480  
Qy 481 RHNERRFLRNTKFIISLGKHAHKLQELTWKMSVRCDAWLRRSPGVCPAAEHLRREEI 540  
Db 481 RHNERRFLRNTKFIISLGKHAHKLQELTWKMSVRCDAWLRRSPGVCPAAEHLRREEI 540  
Qy 541 LAKFLHMLMSVYVVELLRSFYVTTETFOKNRLFYKRSVMSKLOSIGIRQHLKRVOLRE 600  
Db 541 LAKFLHMLMSVYVVELLRSFYVTTETFOKNRLFYKRSVMSKLOSIGIRQHLKRVOLRE 600  
Qy 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVGARTFRREKKAERLTSRVKA 660  
Db 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVGARTFRREKKAERLTSRVKA 660  
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMTFFVLVRAQDPPPELYFVKVDVTGAYDTI 720  
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMTFFVLVRAQDPPPELYFVKVDVTGAYDTI 720  
Qy 721 QDRLTEVIASIIKPNQTYCYRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780  
Db 721 QDRLTEVIASIIKPNQTYCYRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780  
Qy 781 QETSPLDADVIEQSSINEASSGLFDVFLRFMCHHVRIRGKSVYVOCQIGIPQGSILSTL 840  
Db 781 QETSPLDADVIEQSSINEASSGLFDVFLRFMCHHVRIRGKSVYVOCQIGIPQGSILSTL 840  
Qy 841 LCSICYGDMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900  
Db 841 LCSICYGDMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900  
Qy 901 RKTVVNPEVEALGCTAFVQMPAHGLFPWCGLLDTRTLEVDQSDYSYARTSIRASLTIF 960  
Db 901 RKTVVNPEVEALGCTAFVQMPAHGLFPWCGLLDTRTLEVDQSDYSYARTSIRASLTIF 960  
Qy 961 NRGFKAGNMRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020  
Db 961 NRGFKAGNMRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020  
Qy 1021 FHOQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080  
Db 1021 FHOQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080  
Qy 1081 KLTHRRVTVYVPLLSLRTAQTLRSKLPGLTTLTALEAANPALPSPDFKTIID 1132  
Db 1081 KLTHRRVTVYVPLLSLRTAQTLRSKLPGLTTLTALEAANPALPSPDFKTIID 1132

RESULT 13

ABR42384  
ID ABR42384 standard; protein; 1132 AA.  
XX  
AC ABR42384;  
XX  
XX  
DT 11-AUG-2003 (first entry)  
XX  
XX Human telomerase reverse transcriptase.  
DE  
XX Telomerase reverse transcriptase; TERT; enzyme; RNA interference;  
KW short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;  
KW immunosuppressive; antinfertility; fungicide; antiparasitic;  
KW antinflammatory; human; gene therapy.  
XX  
OS Homo sapiens.  
XX  
XX WO2003035667-A2.  
XX  
XX 01-MAY-2003.  
PD  
XX

PF 16-OCT-2002; 2002WO-US033065.  
XX  
PR 22-OCT-2001; 2001US-0345326P.  
PR 20-FEB-2002; 2002US-0359196P.  
PR 22-MAY-2002; 2002US-0383195P.  
XX  
PA (UYRP ) UNIV ROCHESTER.  
XX  
XX Rowley PT;  
PI  
XX  
DR WPI; 2003-403336/38.  
DR N-PSDB; ACC58039.  
XX  
PT Novel double-stranded short interfering RNA having sense and antisense  
PT nucleic acids which are complementary to each other and to target nucleic  
PT acid e.g., telomerase RNA or mRNA encoding telomerase reverse  
PT transcriptase.  
XX  
PS Disclosure; Fig 4; 37pp; English.  
XX  
CC The present sequence is the protein sequence of human telomerase reverse  
CC transcriptase (TERT). The invention relates to the discovery that double-  
CC stranded interfering RNAs, such as short interfering RNAs (siRNA), which  
CC target telomerase RNA or TERT mRNA are capable of inhibiting telomerase  
CC activity. Inhibition of telomerase in cancer cells leads to telomere  
CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of  
CC telomerase activity can also be used for treatment of infertility, for  
CC contraception or sterilisation, for immunosuppression, for treatment of  
CC yeast, parasite and fungal infections, and in anti-inflammatory therapies.  
CC As telomerase is active in a limited number of cell types, e.g. tumour  
CC cells, germline cells, certain stem cells of the haematopoietic system, T  
CC and B cells, sun-damaged skin, and proliferative cervix, most normal  
CC cells are not affected by telomerase RNA interference therapy  
XX  
SQ Sequence 1132 AA;  
Query Match 100.0%; Score 5961; DB 6; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRAPCRVRSLLRSHYREVLPATFVRRLPGQWELVORGDPAAFRALVAOCLVCVPW 60  
Db 1 MPRAPCRVRSLLRSHYREVLPATFVRRLPGQWELVORGDPAAFRALVAOCLVCVPW 60  
Qy 61 DARPPPAAPFROVSCLELVARVLQRLCERGAKNVLAFCGALLDARGCGPPEAFTTSVR 120  
Db 61 DARPPPAAPFROVSCLELVARVLQRLCERGAKNVLAFCGALLDARGCGPPEAFTTSVR 120  
Qy 121 SYLPTNTVDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Db 121 SYLPTNTVDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Qy 181 ATOARPPPHASGPRRLGCRANVHSVREAGVPLGLPAGCARRRGSASRLPLPKPRR 240  
Db 181 ATOARPPPHASGPRRLGCRANVHSVREAGVPLGLPAGCARRRGSASRLPLPKPRR 240  
Qy 241 GAAPEPERTVPGQSWAHPCGTRGPDGFCVVSPPARPAEATSLEGALSGTRHSHPSVG 300  
Db 241 GAAPEPERTVPGQSWAHPCGTRGPDGFCVVSPPARPAEATSLEGALSGTRHSHPSVG 300  
Qy 301 RQHAGPPSTSRPPRMDTFCPPVYATKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360  
Db 301 RQHAGPPSTSRPPRMDTFCPPVYATKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360  
Qy 361 VETIFLGRSPPMPTGTPRRLLPQRYWQMRPLFLELLGNHAQCYPYGVLLKTHCPLRAAVT 420  
Db 361 VETIFLGRSPPMPTGTPRRLLPQRYWQMRPLFLELLGNHAQCYPYGVLLKTHCPLRAAVT 420  
Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSPPQWYGFVRACLRLRLVPPGLWGS 480  
Db 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSPPQWYGFVRACLRLRLVPPGLWGS 480  
Qy 481 RHNERRFLRNTKFIISLGKHAHKLQELTWKMSVRCDAWLRRSPGVCPAAEHLRREEI 540

Db 481 RHNERFLRNTKFTSLGKHAKLSQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540  
QY 541 LAKFLHLMMSVVVVELLSRFFVTTTQKRLFPYKSVMSKLSIGIROHLKRVOLRE 600  
Db 541 LAKFLHLMMSVVVVELLSRFFVTTTQKRLFPYKSVMSKLSIGIROHLKRVOLRE 600  
QY 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660  
Db 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660  
QY 661 LFSVLNFERARRPGLLGASVGLDDIHRAMWTFVLVRADPPPELYFVKVDVTGAYDTI 720  
Db 661 LFSVLNFERARRPGLLGASVGLDDIHRAMWTFVLVRADPPPELYFVKVDVTGAYDTI 720  
QY 721 PQDLRLTEVIASIIKPONTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780  
Db 721 PQDLRLTEVIASIIKPONTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780  
QY 781 QETSPDRDAVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCQIGIPOGSIILSTL 840  
Db 781 QETSPDRDAVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCQIGIPOGSIILSTL 840  
QY 841 LCSLCYGD MENKLFAGIRDRGLLRLVDDFLLVTPHLLTHAKTFTLTLVRGVPYGCVVNL 900  
Db 841 LCSLCYGD MENKLFAGIRDRGLLRLVDDFLLVTPHLLTHAKTFTLTLVRGVPYGCVVNL 900  
QY 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVOSSDYSSYARTSIRASLTF 960  
Db 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVOSSDYSSYARTSIRASLTF 960  
QY 961 NRGFKAGNRMRKLFVLRKCHSLFLDLQVNSLQTVCTNIYKILLIQAAYRPHACVLQLP 1020  
Db 961 NRGFKAGNRMRKLFVLRKCHSLFLDLQVNSLQTVCTNIYKILLIQAAYRPHACVLQLP 1020  
QY 1021 FHOQVKNPTFFLVRISDTSASLCSYILKAKNAGMSLGAKGAGPLPSEAVQWMLCHQAFLL 1080  
Db 1021 FHOQVKNPTFFLVRISDTSASLCSYILKAKNAGMSLGAKGAGPLPSEAVQWMLCHQAFLL 1080  
QY 1081 KLTRHRYVYVPLGLSRLTAQTQLSRKLPGTTLTALEAANPALPSPDKTILD 1132  
Db 1081 KLTRHRYVYVPLGLSRLTAQTQLSRKLPGTTLTALEAANPALPSPDKTILD 1132  
RESULT 14  
ABR42063  
ID ABR42063 standard; protein; 1132 AA.  
XX  
AC ABR42063;  
XX  
DT 28-JUL-2003 (first entry)  
XX  
DE Human telomerase reverse transcriptase.  
XX  
KW Telomerase reverse transcriptase.  
KW short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;  
KW immunosuppressive; antifertility; fungicide; antiparasitic;  
KW antiinflammatory; human; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO2003034985-A2.  
XX  
PD 01-MAY-2003.  
XX  
PF 16-OCT-2002; 2002WO-US033146.  
XX  
PR 22-OCT-2001; 2001US-0345326P.  
PR 20-FEB-2002; 2002US-0359196P.  
PR 22-MAY-2002; 2002US-0383195P.  
XX  
PA (UYRP ) UNIV ROCHESTER.  
XX

PI Rowley PT;

XX  
DR WPI; 2003-403289/38.  
DR N-PSDB; ACC57552.XX  
PT Novel nucleic acid encoding or comprising interfering RNAs which target  
PT telomerase RNA, useful for inhibiting telomerase activity for treating  
PT cancer, infertility and disorders of the immune system.XX  
XX Disclosure; Fig 4; 52pp; English.XX  
XX The present invention is that of human telomerase reverse transcriptase  
XX (TERT). The invention relates to the discovery that double-stranded  
XX interfering RNAs, such as short interfering RNAs (siRNA), which target  
XX telomerase RNA or TERT mRNA are capable of inhibiting telomerase  
XX activity. Inhibition of telomerase in cancer cells leads to telomere  
XX shortening, end-to-end chromosomal fusion, and apoptosis. Interference of  
XX telomerase activity can also be used for treatment of infertility, for  
XX contraception or sterilisation, for immunosuppression, for treatment of  
XX yeast, parasite and fungal infections, and in antiinflammatory therapies.  
XX As telomerase is active in a limited number of cell types, e.g. tumour  
XX cells, germline cells, certain stem cells of the haematopoietic system, T  
XX and B cells, sun-damaged skin, and proliferative cervix, most normal  
XX cells are not affected by telomerase RNA interference therapyXX  
SQ Sequence 1132 AA;Query Match 100.0%; Score 5961; DB 6; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 MPRAPRCAVRSLRSHYREVLPPLATFVRRILGPGQWRILVQRGDPAAAFALVAQCILVCPW 60  
Db 1 MPRAPRCAVRSLRSHYREVLPPLATFVRRILGPGQWRILVQRGDPAAAFALVAQCILVCPW 60  
QY 61 DARPPPAAPSPFQVSKLKVLRVLRQRCERAKNVLAFFGALLDARGGPEAFTTSVR 120  
Db 61 DARPPPAAPSPFQVSKLKVLRVLRQRCERAKNVLAFFGALLDARGGPEAFTTSVR 120  
QY 121 SYLPTNTVDALRGSGAWGLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Db 121 SYLPTNTVDALRGSGAWGLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
QY 181 ATQARPPPHASGPRRRRLCERAWNHSVREAGVPLGLPAGARRRGGSSASRLPLPKRRR 240  
Db 181 ATQARPPPHASGPRRRRLCERAWNHSVREAGVPLGLPAGARRRGGSSASRLPLPKRRR 240  
QY 241 GAAPEPERTVPGQSWAHPPGTRGTPSDRGFCVSPARPAAEATSLGALSCTRHSHPVG 300  
Db 241 GAAPEPERTVPGQSWAHPPGTRGTPSDRGFCVSPARPAAEATSLGALSCTRHSHPVG 300  
QY 301 RQHAGPPSTSRPPRPMDTTPCPVYAEVKHFLYSSGDKQLRPSFLSSLPSTGARRL 360  
Db 301 RQHAGPPSTSRPPRPMDTTPCPVYAEVKHFLYSSGDKQLRPSFLSSLPSTGARRL 360  
QY 361 VETIFLGSRPWPMPGTRELPELPORYQWMPRLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420  
Db 361 VETIFLGSRPWPMPGTRELPELPORYQWMPRLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420  
QY 421 PAAGVCAREKPGQSWAAPEEEDTDPRLVQLLRQHSSPQWVYGFVACLRRLRPPGLWGS 480  
Db 421 PAAGVCAREKPGQSWAAPEEEDTDPRLVQLLRQHSSPQWVYGFVACLRRLRPPGLWGS 480  
QY 481 RHNERFLRNTKFTSLGKHAKLSQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540  
Db 481 RHNERFLRNTKFTSLGKHAKLSQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540  
QY 541 LAKFLHLMMSVVVVELLSRFFVTTTQKRLFPYKSVMSKLSIGIROHLKRVOLRE 600  
Db 541 LAKFLHLMMSVVVVELLSRFFVTTTQKRLFPYKSVMSKLSIGIROHLKRVOLRE 600  
QY 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660  
XX

Db 601 LSEAEVQHQREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERTSRVKA 660  
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720  
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720  
Qy 721 QDRLTEVIAIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780  
Db 721 QDRLTEVIAIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780  
Qy 781 QETSPLRDVAVIEOSSLINEASSGLFDFVLFPMCHAVIRGKSVYVOCQIGIPQGSILSTL 840  
Db 781 QETSPLRDVAVIEOSSLINEASSGLFDFVLFPMCHAVIRGKSVYVOCQIGIPQGSILSTL 840  
Qy 841 LCSLCYGDGMENKLPAGIRRDGLLRLVDDFLLVPHLTHAKTFLRTLVRGVPEYGCVVNL 900  
Db 841 LCSLCYGDGMENKLPAGIRRDGLLRLVDDFLLVPHLTHAKTFLRTLVRGVPEYGCVVNL 900  
Qy 901 RKTVVNPFVEDEALGGTAFVOMPAGHLPFPWCGLLDRTRLEVOQSDYSYARTSRASLTFF 960  
Db 901 RKTVVNPFVEDEALGGTAFVOMPAGHLPFPWCGLLDRTRLEVOQSDYSYARTSRASLTFF 960  
Qy 961 NRGEKAGNRWPKLFGVLRKCHSLFDLDQVNSLOTCTNLYKTLILLQAYRPHACVLQLP 1020  
Db 961 NRGEKAGNRWPKLFGVLRKCHSLFDLDQVNSLOTCTNLYKTLILLQAYRPHACVLQLP 1020  
Qy 1021 FHOQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAPLL 1080  
Db 1021 FHOQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAPLL 1080  
Qy 1081 KLTRHRTVYVPLLSGLRTAQQLSRKLPFGTTLTALAAAAANPALPSDFKTLID 1132  
Db 1081 KLTRHRTVYVPLLSGLRTAQQLSRKLPFGTTLTALAAAAANPALPSDFKTLID 1132  
RESULT 15  
ABP56676  
ID ABP56676 standard; protein; 1132 AA.  
XX  
AC ABP56676;  
XX  
DT 25-MAR-2003 (first entry)  
XX  
DE Human telomerase reverse transcriptase protein SEQ ID NO:2  
XX  
KW Human; telomerase reverse transcriptase; enzyme; hTERT; chromosome 5;  
KW vulnary; antiulcer; epithelial cell migration promoter; wound;  
KW epithelisation; skin wound; lesion; burn; surgical incision; ulcer;  
KW epithelial cell; keratinocyte; epidermal; mucosal.  
XX  
OS Homo sapiens.  
XX  
PN WO200291999-A2.  
XX  
PD 21-NOV-2002.  
XX  
PF 09-MAY-2002; 2002WO-US014867.  
XX  
PR 09-MAY-2001; 2001US-0289903P.  
XX  
PA (GERO-) GERON CORP.  
XX  
PI Jiang X, Chiu C, Harley CB;  
XX  
DR WPI; 2003-120591/11.  
DR N-ESDB; ABZ22474.  
XX  
PT Composition for treating wounds and enhancing epithelization of a skin  
PT surface, comprises vector encoding telomerase reverse transcriptase or  
PT telomerized epithelial cells on a microparticle or a matrix.  
XX  
PS Disclosure; Page 32; 68pp; English.  
XX

CC The present invention describes a pharmaceutical composition (I) comprising a vector encoding telomerase reverse transcriptase (TERT) in an excipient or device, or comprises telomerized epithelial cells on a microparticle or a matrix suitable for topical administration or administration to a wound site. (I) has vulnary and antiulcer activities and can be used to promote epithelial cell migration. (I) is useful for treating a wound and enhancing epithelisation of a skin surface. The wound is especially skin wound including acute lesion such as traumatic lesion, burn, or surgical incision, chronic lesion such as chronic venous ulcer, diabetic ulcer or compression ulcer and the wound is further monitored for closure. The telomerase activity or TERT expression is increased in epithelial cells at the site of treatment and also in fibroblasts or endothelial cells at the site of treatment. The epithelial cells are especially keratinocytes. A polynucleotide encoding TERT is useful for the preparation of a medicament for treatment of a wound or an epithelial surface in a human or animal. An epithelial cell with increased telomerase activity or increased expression of TERT is useful for preparation of a medicament for the treatment of a wound in a human or animal. (I) is also useful for treating wounds of other epidermal surfaces including mucosal surfaces such as bronchus, mouth, nose, oesophagus, stomach, or intestine. The present sequence represents human TERT (hTERT), which is given in the exemplification of the present invention. hTERT is located to chromosome 5  
XX  
SQ Sequence 1132 AA;  
Query Match 100.0%; Score 5961; DB 6; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGQWRLVQRGDPAAFRALVQAQLVCVPM 60  
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGQWRLVQRGDPAAFRALVQAQLVCVPM 60  
Qy 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGALLDARGGPPPEAFTTSVR 120  
Db 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGALLDARGGPPPEAFTTSVR 120  
Qy 121 SYLPTNTVDALRGSGAWGLLRLRVGDDVLVHLARCALFVLVAPSCAYVCGPPLYLQGA 180  
Db 121 SYLPTNTVDALRGSGAWGLLRLRVGDDVLVHLARCALFVLVAPSCAYVCGPPLYLQGA 180  
Qy 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGSASRLPLPKPRR 240  
Db 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGSASRLPLPKPRR 240  
Qy 241 GAPEPERTVQGGSWAHPORTGSDRGFCVVSPPAPAEATSLGALSGTRHSHPSVG 300  
Db 241 GAPEPERTVQGGSWAHPORTGSDRGFCVVSPPAPAEATSLGALSGTRHSHPSVG 300  
Qy 301 RQHHAGPPSTSRPPRPMWDTPCPPVYAEKHFLYSSGDKQELRPSFLSSLRPSLTGARRL 360  
Db 301 RQHHAGPPSTSRPPRPMWDTPCPPVYAEKHFLYSSGDKQELRPSFLSSLRPSLTGARRL 360  
Qy 361 VETIFLGSREPMFCTPRRLPRLPQRYWQMRPLFLELGNHAQCYPGYLLKTHCFLRAAVT 420  
Db 361 VETIFLGSREPMFCTPRRLPRLPQRYWQMRPLFLELGNHAQCYPGYLLKTHCFLRAAVT 420  
Qy 421 PAAGVCAREKPGQSVAAPEBEDTDPRLVOLLRQHSSFPWQYGFVRACLRLVPPGLWGS 480  
Db 421 PAAGVCAREKPGQSVAAPEBEDTDPRLVOLLRQHSSFPWQYGFVRACLRLVPPGLWGS 480  
Qy 481 RHNERFLRNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHLREEI 540  
Db 481 RHNERFLRNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHLREEI 540  
Qy 541 LAKFLHLMVYVVELLSRFFYVTTTFFQKRLFFYRKSVMSKLQSIGIRQHLKRVQURE 600  
Db 541 LAKFLHLMVYVVELLSRFFYVTTTFFQKRLFFYRKSVMSKLQSIGIRQHLKRVQURE 600  
Qy 601 LSEAEVQHQREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERTSRVKA 660  
Db 601 LSEAEVQHQREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERTSRVKA 660

Qy	661	LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQPPPELYFVKVDVTGAYDTI	720
Db	661	LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQPPPELYFVKVDVTGAYDTI	720
Qy	721	PODLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL	780
Db	721	PODLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL	780
Qy	781	QETSPLRDADVIEOSSINEASSGLFDVFLRFMCHHAVIRGKSYVOCQGIPOGSIILSTL	840
Db	781	QETSPLRDADVIEOSSINEASSGLFDVFLRFMCHHAVIRGKSYVOCQGIPOGSIILSTL	840
Qy	841	LCSLCYGD MENKLFAGIRRDG LLRLVDDFLLVTPH LTHAKTFLRTLVRGVPEYGCVVNL	900
Db	841	LCSLCYGD MENKLFAGIRRDG LLRLVDDFLLVTPH LTHAKTFLRTLVRGVPEYGCVVNL	900
Qy	901	RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVOSSDYSSYARTSIRASLTF	960
Db	901	RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVOSSDYSSYARTSIRASLTF	960
Qy	961	NRGFKAGRNMRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP	1020
Db	961	NRGFKAGRNMRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP	1020
Qy	1021	FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL	1080
Db	1021	FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL	1080
Qy	1081	KLTRHRVTVYVPLGSLRTAQTLRSRKLPGTTLTALEAAANPALPSDFKTILD	1132
Db	1081	KLTRHRVTVYVPLGSLRTAQTLRSRKLPGTTLTALEAAANPALPSDFKTILD	1132

Search completed: January 10, 2005, 17:34:53  
Job time : 175 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 10, 2005, 17:22:50 ; Search time 215 Seconds  
(without alignments)  
3029.414 Million cell updates/sec

Title: US-10-053-758-225

Perfect score: 5961

Sequence: 1 MPRAPRCRAVRLSLRSHYRE.....TALEAAANPALPSDFKTILD 1132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5961	100.0	1132	1	TERT_HUMAN	Q14746 homo sapien
2	5583.5	93.7	1069	2	Q8NG46	Q8ng46 homo sapien
3	4052	68.0	807	2	Q8N6C3	Q8n6c3 homo sapien
4	3973	66.6	795	2	Q8NG38	Q8ng38 homo sapien
5	3628	60.9	1128	2	Q8QX24	Q8qx24 mesocricetu
6	3505	58.8	1122	1	TERT_MOUSE	Q70372 mus musculus
7	2825	47.4	524	2	Q9UBR6	Q9ubr6 homo sapien
8	2590	43.4	1346	2	Q6RD80	Q6rd80 gallus gall
9	2590	43.4	1346	2	AA575793	AA575793 gallus ga
10	2316.5	38.9	1191	2	Q9DE32	Q9de32 xenopus lae
11	2207.5	37.0	523	2	Q94807	Q94807 homo sapien
12	2016	33.8	575	2	Q9JK99	Q9jk99 rattus norv
13	1373	23.0	514	2	Q9R266	Q9r266 mus musculus
14	724.5	12.2	1123	2	Q9SE39	Q9se99 arabidopsis
15	724.5	12.2	1123	2	Q9SPU7	Q9spu7 arabidopsis
16	688	11.5	1259	2	Q9AU13	Q9aul13 oryza sativ
17	654.5	11.0	1261	2	Q8LKW0	Q8lkw0 oryza sativ
18	594	10.0	988	1	TERT_SCHPO	Q13339 schizosacch
19	478	8.0	1032	2	Q7Z1L1	Q7z1l1 euplotes cr
20	474	8.0	1032	2	Q8MUB3	Q8mub3 euplotes cr
21	469.5	7.9	939	2	Q7SD71	Q7sd71 neurospora
22	450	7.5	85	2	Q9UNS6	Q9unes6 homo sapien
23	450	7.5	940	2	Q8C9D0	Q8c9d0 yarrowia li
24	449	7.5	116	2	Q8OSU5	Q8osu5 rattus norv
25	448.5	7.5	1031	1	TERT_EUPAE	Q00939 euplotes ae
26	441	7.4	1032	2	Q7Z1L0	Q7z1l0 euplotes cr
27	408	6.8	823	2	Q8SQ00	Q8sq00 encephalito
28	397	6.7	104	2	Q9JLM1	Q9jlm1 mus musculus
29	395.5	6.6	1135	2	Q8I8Z7	Q8i8z7 sterkiella
30	395	6.6	1132	1	TERT_OXYTR	Q76332 oxytricha t
31	395	6.6	1132	2	AA87865	AA87865 sterkiell

32	394	6.6	73	2	Q9UNR4	Q9unr4 homo sapien
33	392	6.6	1108	2	Q8I8Z6	Q8i8z6 sterkiella
34	389.5	6.5	861	2	Q6CS00	Q6cs00 kluyveromyc
35	365	6.1	867	2	Q9P8T3	Q9p8t3 candida alb
36	364	6.1	895	2	Q9GR05	Q9gr05 paramecium
37	363	6.1	1117	1	TERT_TETTH	Q77448 tetrahymena
38	361	6.1	867	2	Q9P8T2	Q9p8t2 candida alb
39	356.5	6.0	884	1	TERT_YEAST	Q6163 saccharomyc
40	355.5	6.0	894	2	Q6BUF6	Q6buf6 debaryomyc
41	342	5.7	896	2	Q8MUQ8	Q8muq8 paramecium
42	339	5.7	79	2	Q7YR69	Q7yr69 felis silve
43	338	5.7	79	2	Q76K45	Q76k45 canis famil
44	338	5.7	79	2	BAD06179	Bad06179 canis fam
45	320	5.4	853	2	Q752S9	Q752s9 ashbya goss

ALIGNMENTS

RESULT 1

ID	TERT_HUMAN	STANDARD;	PRT;	1132 AA.
AC	Q14746: Q14783;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (HST12) (Telomerase-associated protein 2) (TP2).			
DE	Name=TERT; Synonyms=TRT, EST2, TCS1;			
GN	Homo sapiens (Human)			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RC	TISSUE=Kidney; PubMed=9252327;			
RX	MEDLINE=97400623; PubMed=9252327;			
RA	Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H.,			
RA	Lingner J., Harley C.B., Cech T.R.;			
RT	"Telomerase catalytic subunit homologs from fission yeast and human.";			
RL	Science 277:955-959(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97433088; PubMed=9288757;			
RA	Meyerson M., Counter C.M., Eaton E.N., Ellisen L.W., Steiner P.,			
RA	Caddle S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu Q.,			
RA	Bacchetti S., Haber D.A., Weinberg R.A.;			
RT	"hEST2, the putative human telomerase catalytic subunit gene, is up-			
RT	regulated in tumor cells and during immortalization.";			
RL	Cell 90:785-795(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99267414; PubMed=10333526;			
RA	Wick M., Zubov D., Hagen G.;			
RT	"Genomic organization and promoter characterization of the gene			
RT	encoding the human telomerase reverse transcriptase (hTERT).";			
RL	Gene 232:97-106(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Londono-Vallejo J.A.;			
RT	"Sequence of a BAC carrying the entire hTERT gene.";			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	FUNCTION IN TELOMERASE ACTIVITY, TISSUE SPECIFICITY, ASSOCIATION WITH			
RP	TEP1, AND MUTAGENESIS OF ASP-868; ASP-869 AND ASP-712.			
RX	PubMed=9389643;			
RA	Harrington L., Zhou W., McPhail T., Oulton R., Yeung D.S., Mar V.,			
RA	Bass M.B., Robinson M.O.;			
RT	"Human telomerase contains evolutionarily conserved catalytic and			
RT	structural subunits.";			
RL	Genes Dev. 11:3109-3115(1997).			
RN	[6]			
RP	ASSOCIATION WITH TEP1.			

```

RX PubMed=11029039;
RA Beattie T.L., Zhou W., Robinson M.O., Harrington L.;
RT "Polymerization defects within human telomerase are distinct from
RL telomerase RNA and TEPI binding.";
RL Mol. Biol. Cell 11.3329-3340(2000).
CC -1- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
CC the replication of chromosome termini in most eukaryotes. It
CC elongates telomeres. It is a reverse transcriptase that adds
CC simple sequence repeats to chromosome ends by copying a template
CC sequence within the RNA component of the enzyme.
CC -1- SUBUNIT: Component of the telomerase ribonucleoprotein complex at
CC least composed of TEPI, EST1A, POT1 and a telomerase RNA template
CC component (TER). Interacts with PINX1.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: Activation and cancer cell pathogenesis.
CC immortalization and cancer cell pathogenesis.
CC -1- SIMILARITY: Belongs to the reverse transcriptase family.
CC Telomerase subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@sib-ebi.ch).
CC -----
CC EMBL; AF015950; AAC51672.1; -.
CC EMBL; AF018167; AAC51724.1; -.
CC EMBL; AF128894; AAB30037.1; -.
CC EMBL; AF128893; AAB30037.1; JOINED.
CC EMBL; AY007685; AAG23289.1; -.
CC PIR; T03844; T03844.
CC Genew; HGNC:11730; TERT.
CC MIM; 187270; -.
CC GO; GO:000781; C:chromosome, telomeric region; TAS.
CC GO; GO:0042162; F:telomeric DNA binding; TAS.
CC DR; GO:0003721; F:telomeric template RNA reverse transcriptase. .; TAS.
CC InterPro; IPR000477; RVTse.
CC InterPro; IPR003545; Telomerase_RT.
CC Pfam; PF00078; RVT; 1.
CC PRINTS; PR01365; TELOMERASERT.
CC RNA-binding; Nuclear protein; Ribonucleoprotein;
CC RNA-directed DNA polymerase; Telomere; Transferrase.
CC MUTAGEN 868 868 D->A: Loss of telomerase activity.
CC FT MUTAGEN 868 869 DD->AA: Loss of telomerase activity.
CC FT MUTAGEN 869 869 D->A: Loss of telomerase activity.
CC FT MUTAGEN 712 712 D->A: Loss of telomerase activity.
CC FT CONFLICT 516 516 D -> G (in Ref. 2).
CC SQ SEQUENCE 1132 AA; 126996 MW; 94E35469C4CA33A0 CRC64;

Query Match 100.0%; Score 5961; DB 1; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLGQGWRLVQRGDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLGQGWRLVQRGDPAAFRALVAQCLVCVPW 60
QY 61 DARRPPAAPSPROVSCIKELVARVLQRLCERGAKNVLAFAFALLDARGGPPFAFTTSVR 120
Db 61 DARRPPAAPSPROVSCIKELVARVLQRLCERGAKNVLAFAFALLDARGGPPFAFTTSVR 120
QY 121 SYLPTNTVTDALRGSGAWGLLRVGGDVLVHLLARCAFLVLPAPSCAYQVCGPPLVOLGA 180
Db 121 SYLPTNTVTDALRGSGAWGLLRVGGDVLVHLLARCAFLVLPAPSCAYQVCGPPLVOLGA 180
QY 181 ATQARPPPHASGPRRLGCRANVHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPR 240
Db 181 ATQARPPPHASGPRRLGCRANVHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPR 240
QY 241 GAAPPEPTPVGQGSWAHPQTRGPSDRGFCVVSPARPABEATSLGALSSTGRHSPSVG 300

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Db 241 GAAPPEPTPVGQGSWAHPQTRGPSDRGFCVVSPARPABEATSLGALSSTGRHSPSVG 300
QY 301 RQHHAGPPSTSRPRPDWTPCPVYAETHFLYSSGDKQLRPSFLLSSLRPSLTGARRL 360
Db 301 RQHHAGPPSTSRPRPDWTPCPVYAETHFLYSSGDKQLRPSFLLSSLRPSLTGARRL 360
QY 361 VETIFLGSRPWMEGTTPRRLPRLPQRYWQMRPFLLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPWMEGTTPRRLPRLPQRYWQMRPFLLELLGNHAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPKQGSVAAPBEEDTPRRLVOLLRQHSSPWQYGFVRACLRRLLVPPGLWGS 480
Db 421 PAAGVCAREKPKQGSVAAPBEEDTPRRLVOLLRQHSSPWQYGFVRACLRRLLVPPGLWGS 480
QY 481 RHNERFLRNTKKFISLGKHAKLSQLTWMKSVRDCAMLRSPGVCVGAASHRRLREEI 540
Db 481 RHNERFLRNTKKFISLGKHAKLSQLTWMKSVRDCAMLRSPGVCVGAASHRRLREEI 540
QY 541 LAKFLHMLSVVYVVELLRSEFFVYVTTTFQKNRLFYFKSVWSKLQSIGIRQHILKRVQLRE 600
Db 541 LAKFLHMLSVVYVVELLRSEFFVYVTTTFQKNRLFYFKSVWSKLQSIGIRQHILKRVQLRE 600
QY 601 LSEAEVQRHREARPPALLTSRLRPIPKPDGLRPIVNNMDYVVGARTFRREKRAEELTSRVKA 660
Db 601 LSEAEVQRHREARPPALLTSRLRPIPKPDGLRPIVNNMDYVVGARTFRREKRAEELTSRVKA 660
QY 661 LFSVLNVERARRPGLLGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRFKSHVSTLTLDLQPYMRQFVAHL 780
Db 721 PDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRFKSHVSTLTLDLQPYMRQFVAHL 780
QY 781 QETSPLRDADVIEQSSSLNEASGLPDVFLRPFCHHVRIRGKSVYVQCOGIPGSGILSTL 840
Db 781 QETSPLRDADVIEQSSSLNEASGLPDVFLRPFCHHVRIRGKSVYVQCOGIPGSGILSTL 840
QY 841 LCSLCYGDWENKLFAGIRDDGLLLRLVDDFLVTLPHLTHAKTFLRTLVRGVPEYGCVVNL 900
Db 841 LCSLCYGDWENKLFAGIRDDGLLLRLVDDFLVTLPHLTHAKTFLRTLVRGVPEYGCVVNL 900
QY 901 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDTLRTLVEQSDYSSVARTSIRASLTF 960
Db 901 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDTLRTLVEQSDYSSVARTSIRASLTF 960
QY 961 NRGFKAGRNMRKLFQVLRBLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGRNMRKLFQVLRBLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
QY 1021 FHOQVWKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHOAFL 1080
Db 1021 FHOQVWKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHOAFL 1080
QY 1081 KLTRHRTVTVPLGLSLRTAQTLQSRKLPGLTTLTALEAAANPALPSDFKTLTD 1132
Db 1081 KLTRHRTVTVPLGLSLRTAQTLQSRKLPGLTTLTALEAAANPALPSDFKTLTD 1132

RESULT 2
Q8NG46 PRELIMINARY; PRT; 1069 AA.
ID Q8NG46;
AC Q8NG46;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Telomerase reverse transcriptase.
GN Name=hTERT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```

RP SEQUENCE FROM N.A.  
RA Hisatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB085628; BAC11010.1; -.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.  
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.  
DR InterPro; IPR003545; Telomerase\_RT.  
DR PRINTS; PR01365; TELOMERASERT.  
DR RNA-directed DNA polymerase.  
KW SEQUENCE 1069 AA; 120046 MW; BE1E77A653B1C666 CRC64;  
SQ  
Query Match 93.7%; Score 5583.5; DB 2; Length 1069;  
Best Local Similarity 94.4%; Pred. No. 0;  
Matches 1069; Conservative 0; Mismatches 0; Indels 63; Gaps 1;  
Qy 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLPGQWRLVORGDPAAFALVAQCLVCVPW 60  
Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLPGQWRLVORGDPAAFALVAQCLVCVPW 60  
Qy 61 DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGAGGPEAFTTSVR 120  
Db 61 DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGAGGPEAFTTSVR 120  
Qy 121 SYLNTVTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Db 121 SYLNTVTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Qy 181 ATQARPPPHASGPRRRLLCGERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRRR 240  
Db 181 ATQARPPPHASGPRRRLLCGERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRRR 240  
Qy 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSILEGALSGTRHSHPSVG 300  
Db 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSILEGALSGTRHSHPSVG 300  
Qy 301 RQHAGPPSTSRPPMDTPCPVVAETKHFLLYSSGDKQELRPSFLLSLSPSLTGARRL 360  
Db 301 RQHAGPPSTSRPPMDTPCPVVAETKHFLLYSSGDKQELRPSFLLSLSPSLTGARRL 360  
Qy 361 VETIFLGSRPMWPTPRRLPLPORYWQMRPLFLLELGNHQAQCYGVLLKTHCPLEAAVT 420  
Db 361 VETIFLGSRPMWPTPRRLPLPORYWQMRPLFLLELGNHQAQCYGVLLKTHCPLEAAVT 420  
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPWQYGFVRACLRRLVPPGLWGS 480  
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPWQYGFVRACLRRLVPPGLWGS 480  
Qy 481 RHNERRRFLNTKFTISLGKHAQLSLQELTWQMSVRDCAWLRRSPGVGCPVAAEHLREEI 540  
Db 481 RHNERRRFLNTKFTISLGKHAQLSLQELTWQMSVRDCAWLRRSPGVGCPVAAEHLREEI 540  
Qy 541 LAKPLHLWMSYVVVELLRSPFYVTETTFQKNRLFFYRKSVMSKLSQSIGIRHLKRVQLE 600  
Db 541 LAKPLHLWMSYVVVELLRSPFYVTETTFQKNRLFFYRKSVMSKLSQSIGIRHLKRVQLE 600  
Qy 601 LSEAEVQHRARPALLTSRLRFIPKPDGLPIVNM DYVVCARTFREKRAERLTSRVKA 660  
Db 601 LSEAEVQHRARPALLTSRLRFIPKPDGLPIVNM DYVVCARTFREKRAERLTSRVKA 660  
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWTFFVLVRAQDPPPELVFKVDVDTGAYDTI 720  
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWTFFVLVRAQDPPPELVFKVDVDTGAYDTI 720  
Qy 721 QDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780  
Db 721 QDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780  
Qy 781 QETSPLRDAAVIEOSSSNEASSGLFDVFLRFPMCHAVRIRGKSYVQCQGIPOQSII STL 840  
Db 781 QETSPLRDAAVIEOSSSNEASSGLFDVFLRFPMCHAVRIRGKSYVQCQGIPOQSII STL 840

Qy 841 LCSLCYGD MENKULFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFURTLVRGVPYGVVNL 900  
Db 841 LCSLCYGD MENKULFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFURTLVRGVPYGVVNL 900  
Qy 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEBVQSDYSYARTSIRASLTF 960  
Db 885 -----SYARTSIRASLTF 960  
Qy 961 NRGFKAGNRMRRLFGVRLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020  
Db 898 NRGFKAGNRMRRLFGVRLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 957  
Qy 1021 FHOQVWKNPFTFLRAVISDTASLCYSILKAKNAGNSLGAAGAGPLPSEAVOWLCHQAFLL 1080  
Db 958 FHOQVWKNPFTFLRAVISDTASLCYSILKAKNAGNSLGAAGAGPLPSEAVOWLCHQAFLL 1017  
Qy 1081 KLTHRRVTVYVPLGLSLRTAQTQLSRKLP GTTTLTALEAANPALPSDFKTIID 1132  
Db 1018 KLTHRRVTVYVPLGLSLRTAQTQLSRKLP GTTTLTALEAANPALPSDFKTIID 1069  
RESULT 3  
Q8N6C3 PRELIMINARY; PRT; 807 AA.  
ID Q8N6C3 AC Q8N6C3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Beta and gamma deletion isoform of telomerase reverse transcriptase.  
GN Name=hTERT;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUS=Gastric cancer;  
RA Hisatomi H., Nagao K., Kanamaru T., Sumida H., Hirata H., Yamamoto M.,  
RA Kazumasa H.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB086379; BAC11014.1; -.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.  
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.  
DR InterPro; IPR003545; Telomerase\_RT.  
DR PRINTS; PR01365; TELOMERASERT.  
KW RNA-directed DNA polymerase.  
SQ SEQUENCE 807 AA; 90225 MW; 199664460CE6D763 CRC64;  
Query Match 68.0%; Score 4052; DB 2; Length 807;  
Best Local Similarity 100.0%; Pred. No. 9e-245;  
Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLPGQWRLVORGDPAAFALVAQCLVCVPW 60  
Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLPGQWRLVORGDPAAFALVAQCLVCVPW 60  
Qy 61 DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGAGGPEAFTTSVR 120  
Db 61 DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGAGGPEAFTTSVR 120  
Qy 121 SYLNTVTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Db 121 SYLNTVTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Qy 181 ATQARPPPHASGPRRRLLCGERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRRR 240  
Db 181 ATQARPPPHASGPRRRLLCGERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRRR 240  
Qy 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSILEGALSGTRHSHPSVG 300  
Db 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSILEGALSGTRHSHPSVG 300

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Db 241 GAAPEPERTPVGGSWAHPRTRGSDRGFCVVSPPARPAEEATSLEGALSCTRSHSPSVG 300
Qy 301 RQHAGPSTSRPPRPWDTPCPVYAEAKHFLYSSGDKQELRPSFLSSLRPSLTGARRL 360
Db 301 RQHAGPSTSRPPRPWDTPCPVYAEAKHFLYSSGDKQELRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSWAAPPEEDTDPRRLVQLLRQHSSPMQVYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSWAAPPEEDTDPRRLVQLLRQHSSPMQVYGFVRACLRRLVPPGLWGS 480
Qy 481 RHNERFLRNKTKFISLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERFLRNKTKFISLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
Qy 541 LAKFLHLMMSVYVVELLRSFFVTTTFOKNRLFYRKSVMSKLSQSIGIRQHLKRVQRE 600
Db 541 LAKFLHLMMSVYVVELLRSFFVTTTFOKNRLFYRKSVMSKLSQSIGIRQHLKRVQRE 600
Qy 601 LSEAEVRQREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNVERARRPGLLGASVLGLDDIHRWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763
Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763

RESULT 4
Q8NG38 PRELIMINARY; PRT; 795 AA.
ID Q8NG38 AC Q8NG38;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABG-deleted variant of telomerase reverse transcriptase.
GN Name=TERT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Hisatomi H., Nagao K., Kanamaru T., Hirata H., Miyachi K., Hikiji H.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086950; BAC11015.1; -.
DR GO; GO:0005634; G:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; IEA.
DR InterPro; IPR003545; Telomerase_Rt.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 795 AA; 88964 MW; 6BEAC8A6D1A2E8CB CRC64;

Query Match 66.6%; Score 3973; DB 2; Length 795;
Best Local Similarity 98.4%; Pred. No. 7.7e-240;
Matches 751; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

Qy 1 MPRAPRCRVRSLRSHYREVLPLATFVRRLFGQWRNVQGDPAAFRALVACQVCVFW 60
Db 1 MPRAPRCRVRSLRSHYREVLPLATFVRRLFGQWRNVQGDPAAFRALVACQVCVFW 60
Qy 61 DARPPPAAPSPROVSCIKELVARVLQELCERGAKNVLAFCFALLDARGGPPFAFTTSVR 120
Db 61 DARPPPAAPSPROVSCIKELVARVLQELCERGAKNVLAFCFALLDARGGPPFAFTTSVR 120
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Db 61 DARPPPAAPSPROVSCIKELVARVLQELCERGAKNVLAFCFALLDARGGPPFAFTTSVR 120
Qy 121 SYLPNTVTDALRGSGAWGLLRRVGGDVLVHLIARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLRRVGGDVLVHLIARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPCARRRGGSASRSLPLPKPRR 240
Db 181 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPCARRRGGSASRSLPLPKPRR 240
Qy 241 GAAPEPERTPVGGSWAHPRTRGSDRGFCVVSPPARPAEEATSLEGALSCTRSHSPSVG 300
Db 241 GAAPEPERTPVGGSWAHPRTRGSDRGFCVVSPPARPAEEATSLEGALSCTRSHSPSVG 300
Qy 301 RQHAGPSTSRPPRPWDTPCPVYAEAKHFLYSSGDKQELRPSFLSSLRPSLTGARRL 360
Db 301 RQHAGPSTSRPPRPWDTPCPVYAEAKHFLYSSGDKQELRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSWAAPPEEDTDPRRLVQLLRQHSSPMQVYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSWAAPPEEDTDPRRLVQLLRQHSSPMQVYGFVRACLRRLVPPGLWGS 480
Qy 481 RHNERFLRNKTKFISLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERFLRNKTKFISLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
Qy 541 LAKFLHLMMSVYVVELLRSFFVTTTFOKNRLFYRKSVMSKLSQSIGIRQHLKRVQRE 600
Db 541 LAKFLHLMMSVYVVELLRSFFVTTTFOKNRLFYRKSVMSKLSQSIGIRQHLKRVQRE 600
Qy 601 LSEAEVRQREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNVERARRPGLLGASVLGLDDIHRWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763
Db 711 --DRUTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 751

RESULT 5
Q9QXZ4 PRELIMINARY; PRT; 1128 AA.
ID Q9QXZ4 AC Q9QXZ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Telomerase catalytic subunit.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21240330; PubMed=11342218;
RA Guo W., Okamoto M., Lee Y.M., Baluda M.A., Park N.H.;
RT "Enhanced activity of cloned hamster TERT gene promoter in transformed
cells.";
RL Biochim. Biophys. Acta 1517:398-409 (2001).
DR EMBL; AF149012; AAF17334.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; IEA.
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Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPGQWRVLVQRGDDPAAPRALVAQCLVCVPW	60						
Db	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPGQWRVLVQRGDDPAAPRALVAQCLVCVPW	60						
Qy	61	DARPPPAAPSQVSCLELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVR	120						
Db	61	DARPPPAAPSQVSCLELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVR	120						
Qy	121	SYLNTVTDALRGSGAGLLRRVCGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA	180						
Db	121	SYLNTVTDALRGSGAGLLRRVCGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA	180						
Qy	181	ATOARPPHAGSPRRRLRCERAMNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPRR	240						
Db	181	ATOARPPHAGSPRRRLRCERAMNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPRR	240						
Qy	241	GAAPEPERTPVQGSWAHPGTRGSDRGFCVWSPAPAEATSLLEGALSGTRHSHPSVG	300						
Db	241	GAAPEPERTPVQGSWAHPGTRGSDRGFCVWSPAPAEATSLLEGALSGTRHSHPSVG	300						
Qy	301	ROHAGPSTSRPDPMDTCCPPVYAEKHFYSSGDKQQLRPSFLISSLRPSLTGARRL	360						
Db	301	ROHAGPSTSRPDPMDTCCPPVYAEKHFYSSGDKQQLRPSFLISSLRPSLTGARRL	360						
Qy	361	VETIFLGRSPPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT	420						
Db	361	VETIFLGRSPPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT	420						
Qy	421	PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRHSSPWQYGVFVRACLRRLVPPGLWGS	480						
Db	421	PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRHSSPWQYGVFVRACLRRLVPPGLWGS	480						
Qy	481	RHNERFLRNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRRSP	524						
Db	481	RHNERFLRNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRRSP	524						
RESULT 8									
Q6RD80	ID	Q6RD80	PRELIMINARY; PRT; 1346 AA.						
AC	Q6RD80;								
DT	05-JUL-2004 (TrEMBLrel. 27, Created)								
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)								
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)								
DE	Telomerase reverse transcriptase.								
GN	Name=TERT;								
OS	Gallus gallus gallus.								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;								
OC	Gallus.								
OX	NCBI_TaxID=208526;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RA	Delany M.E., Daniels L.M.;								
RL	Submitted (DSC-2003) to the EMBL/GenBank/DBAJ databases.								
DR	EMBL; AY502592; AAS75793.1; -								
DR	GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.								
DR	InterPro; IPR003545; Telomerase_RT.								
DR	PRINTS; PR01365; TELOMERASERT.								
KW	RNA-directed DNA polymerase.								
SQ	SEQUENCE 1346 AA; 155316 MW; E93A8B64FB6A4D40 CRC64;								
Query Match 43.4%; Score 2590; DB 2; Length 1346;									
Best Local Similarity 44.1%; Pred. No. 4.5e-153;									
Matches 593; Conservative 159; Mismatches 350; Indels 242; Gaps 29;									
Qy	9	AVRSLRSHYREVLPLATFVRL--GPGWRLVORGDDPAAPRALVAQCLVCVPWDARPP	65						
Db	25	AVLGALRGCYAEXTPLFAFVRLRQEGGTGEVFLRGDDAQCYRTFVSCVVCVRGARAI	84						
Qy	66	PAAPSFQVSCLELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVRSVLPN	125						

Db	85	PRPICFOQLSSQSEVITRIVQRLCEKKKNILAYGSLDENSCHFRVLPSSCYSYLSN	144						
Qy	126	TVTDALRGSGAGLLRRVCGDDVLVHLLARCALFVLVAPSCAYOVCPPLVOLGNATQAR	185						
Db	145	TVTETIRISGLWEILLRIGDDVMYLLLEHCALFMLVPPSNICYVCGQPIYEL-TSRNVG	203						
Qy	186	PPP-----HAS---GPRRRLCERAMNHSVREAGVPLGLPAPGARRRGSGASR-	230						
Db	204	PSPGFVRRYSRFXHNSLLDYVRKLVFHR---HYLSKSWMKCRP-----RRGRVSSRR	256						
Qy	231	-----SLPLP-----KRPRGAA	243						
Db	257	KRRSHRISQSLRSGYQPSAKVNFQARQISTVTARLEKQSCSSCLPARAPSLKRKRDEQ	316						
Qy	244	PE-----PERTPVGG-----SW-----	256						
Db	317	VEITAKRVKMEKEIEQACSIVPD---VNSSQRHGTSWHVAPRAVGLIKEHYISERS	373						
Qy	257	-----AHPGR-----TRG-----	264						
Db	374	NSEMSGSVVHRSHPGKRPVADKSSFQGVQGNKRIKTGAEKRAESNRGIEMYINPIHK	433						
Qy	265	PSDRGP-CVVSPPAPAE-----EATSLLEGALSGTRHSHPSVGRQHHAGGPSTSRP	319						
Db	434	PNRRGIERINPTHKPELNSVQTEPMEGASGDRKQE-----NPPAHLAKQLPNTL	484						
Qy	320	PCPPVYAEKHFYSSGDKQQLRPSFLISSLRPSLTGARRLVETIFLGSRPW-----M	372						
Db	485	SRSVTYFEKPLLSYSQYEFPKSFILSRLOCGQAGRRLIETIFUSQNLKQSQNOQL	544						
Qy	373	PGTPRRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCP-----LRAA	418						
Db	545	PQQWRKKRLPKRYWQMREIFQKLVKNHEKCPYLVLKKNKCPVLLSEACKKTELTLQAA	604						
Qy	419	VTAAAGV-----CAREKPG-----SVAA---PEE-----EDTDPRRLVQLLRQ	454						
Db	605	LPGEAKVHKTEHGKSTEGTAPNSFLAPSVLACGQPERGEQHPAESDP-LLELLRQ	663						
Qy	455	HSSPWQYGVFVRACLRRLVPPGLWGRHNERFLRNTKKFISLGKHAKLISLOELTWKMSV	514						
Db	664	HSHWQYGVFVRECLERVI PAELWGSSHNKCRFFFNKVKAFISMKGAKLSLOQLMKMRV	723						
Qy	515	RDCAWLRRSPGVCVPAAEHRLREILAKFLHMLMSVYVVELLSRFFVVTETTFOKNRLF	574						
Db	724	NDCVWLAKGNHSPVAYEHCYREIILAKFLYWLMDSVIELLSKSFYITETMQKMLF	783						
Qy	575	FYRKSVMKLSQSIGIROHLKRVQLRELSAEAFVROHREARPALLTSRLRFIPKPDGLRPV	634						
Db	784	YRKFYWGKLQNIIGIRDHFAKHLRALSSSEMEVIRQKYPPIASRLRFIPKMGRLRPV	843						
Qy	635	NMDYVVGARTF---RREKRAERLTSRVKALFSLVNLNERARRPGLLGASVLGDDIHRAWR	691						
Db	844	RLSRVBEQKLSKESREKKIQRVNTQKLNFLSVNLNERTVNTSIGSVFGRDRIYRKWK	903						
Qy	692	TFVLRV-RAQDPPPELYFVVDVTGAYDTTIPODRLTELVIAIIKP--QNTYCVRYAVVQ	748						
Db	904	EFVTKVFESEGGEMPHFYFVKGDVSRAFTTIPHKLVLEVISQVLKPESTQVYGIWYAVIM	963						
Qy	749	KAAGHVRKAPKSHVSTLTDLPQYMRQFVAHLQETSPLRDVAVTEQSSSLNEASSGLPDV	808						
Db	964	ITPTGKARKLYKRVHSTFEDFIPDMKQFVSKLQERTSLRNAIVVEQCLTFNENSTLPTF	1023						
Qy	809	FLRPMCHAVRIRKSVVQCGIIPQGSILSTLLCSLCYGMENKLFAGIRRDGLLLRLVD	868						
Db	1024	FLQMLHNNLEIGHRYIQCISGIPQGSILSTLLCSLCYGMENKLLCGIQKDGVLIRLID	1083						
Qy	869	DELLVTPHLTHAKTFLRLTVRGVPEYGCVNLRKTVNFPVEDEALGTAFCVQPAHGLF	928						
Db	1084	DFLLVTPHLMQARTFLRTIAGIPEYGFLLNAKTVNFPV-DDIPGSKFKHLPDCCKLI	1142						
Qy	929	PWCGLLDTTLTVQSDYSYVARTSIRASLTFRNGFKAGRNMRKLFVGLRKCHSLFLD	988						



Db 1143 SMCGLLDVQTLLEVYCDYSSAFTSIRSSLSFNSRIAGKNNCKLTAVLKLKCHPLLD 1202  
QY 989 LQVNSLQVCTNIVYKILLQAVRFHACVLQLPFHQVWKNPTFFLRVSDTASLCYSILK 1048  
Db 1203 LKINSLOVVLINIKYIFLLQAVRFHACVLQFPNOKVRNPDFFLRISDTSACCYFLK 1262  
QY 1049 AKNAGMSLGAAGAAGPLPSEAVQWLCFOAFLLKLTTRHRTVTVPLIGSLRTAQOLSRKLP 1108  
Db 1263 AKNPGVSLGSDASGMFFPEAAEWLCYHAFIVKLSNKHVYKCLLKPLKYVMHLLFGKIP 1322  
QY 1109 GTTLTALAANAANPALPSDFKTLID 1132  
Db 1323 RDTMELLKTVPTEPSLCQDFKTLID 1346

RESULT 9  
AAS75793  
ID AAS75793 PRELIMINARY; PRT; 1346 AA.  
AC AAS75793;  
DT 31-MAR-2004 (TremBLrel. 27, Created)  
DT 31-MAR-2004 (TremBLrel. 27, Last sequence update)  
DE Telomerase reverse transcriptase.  
GN TERT.  
OS Gallus gallus gallus.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus; Gallus gallus.  
OX NCBI\_TaxID=208526;  
RN [1]\_TaxID=208526;  
RP SEQUENCE FROM N.A.  
RA Delany M.E., Daniels L.M.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY502592; AAS75793.1; --  
KW RNA-directed DNA polymerase.  
SQ SEQUENCE 1346 AA; 155316 MW; E93A8B64FB6A4D40 CRC64;

Query Match 43.4%; Score 2590; DB 2; Length 1346;  
Best Local Similarity 44.1%; Pred. No. 4.5e-153;  
Matches 593; Conservative 159; Mismatches 350; Indels 242; Gaps 29;

QY 9 AVRSLLRSHYREVLPLATFVRL--GPGWRLVORGDA-AFRALVAQCLVCPWDARPP 65  
Db 25 AVLGAALRGYAEVTPLEAFVRLQEGGTGEVLRGDDAQCYRTFVSCVVCVPRGARAI 84  
QY 66 PAAPSFQVSCLELVARVLQRLCERGAKNVLAFFGALLDGAAGPPEATTSVRSVLPN 125  
Db 85 PRPICFOQLSQSSEVITRIVQRLCEKKKNILAYGSLDENSCHPVLPSFCISYLSN 144  
QY 126 TVTDALRGSGAWGLLRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGAATQAR 185  
Db 145 TVTETIRISGLWEILLRIGDDVMYLLHLCALFMLVPPSNVCYVCGQPIYEL-ISRNVG 203  
QY 186 PPP-----HAS---GPRRLCERAWHSVREAGVPLGLPAGARRGGGSASR- 230  
Db 204 PSPGFVRRYRSRFRKNSLLDVRKRLVFHR---HYLSKQWVKCRP-----RRRGRVSSRR 256  
QY 231 -----SLPLP-----KRPRGAA 243  
Db 257 KRSHRITQSLRSGVQPSAKVNFQNGROIQSTVTARLEKQSCSSLCPLPARPSLKRKRDEQ 316  
QY 244 PE-----PERTPVQGG-----SW----- 256  
Db 317 VEITAKRVKIMEKEIEBQACSIVPD---VNQSSQRHGTSWHVAPRAVGLIKEHYISERS 373  
QY 257 -----AHPGR-----TRG----- 264  
Db 374 NSEMSGPSVHRHGRKPRFVADKSSFPQVQGNKRIKTGAERKAENRRGIEYINPIHK 433  
QY 265 PSDRGF-CVVSPPARPAE-----EATSLGALSGTRHSHPSVGRQHGHAPPSTSRPPPMWT 319  
Db 434 PNRRIERRINPTHKPELNSVQTEPMEGASSGDRKQE-----NPPAHLAKQLPNTL 484

QY 320 PCBPVYAEKTHFLYSSDDKEQLRPSFLSSLSRSLTGARRLVETIFLGSRPW-----M 372  
Db 485 SRSTVYFEKFLYLSRSYQYFPKSFILSRLOQCAGGRRLIETIFLSQPLKEQQNSL 544  
QY 373 PGTPRRRLPRLPQRYWQWRPLFLELLGNHACQPYGVLLKTHCP-----LRAA 418  
Db 545 PQQWRKRRLPQRYWQWRPLFQKLVKHKCPYLFLRKNCPVLLSEACUKKTELTLQAA 604  
QY 419 VTPAAGV-----CAREKPGQ-----SVAA-----PEE-----EDTDPRLRLVQLLRQ 454  
Db 605 LPGEAKVHKHTEHGKESTEGTAPNSFLAPPSVLACQPERGEQHPAEGSDP-LLRELLRQ 663  
QY 455 HSSPQWYGFVRACLRRLVPPGLWGRHRRERLNTKKFISLGKHAUKLSQBLTWMSV 514  
Db 664 HSSHQWYGFVRECLERVIPAEALWSSHNKCRFFKNVKAFISMGKYAKLSLQQLMMKRV 723  
QY 515 RDCAWLRRSPGVCVPAAEHRLREELAKFLHLMSSVYVVELLRSFFYVETTFQKNRLF 574  
Db 724 NDCVWLRLAKGNHVSFAYEHCYREELAKFLYLMDSYVIELKSFYVETTFQKNMLF 783  
QY 575 FYKSVMSKLQSIGIRQHLKRVOLRELSAEVQHREARPALTSRLRFPKPDGLRPV 634  
Db 784 YRKFTWGLQNIQIRDHFAKVHLRALSSSEMEVIRQKVFPIASRLRFPKMWGLRPV 843  
QY 635 NMDYVVGARTF---REEKRAERLTSRVKALFSVLNAYERARRPGLLGASVLGLDDIHRWR 691  
Db 844 RLSRVVEGOKLSKESREKIQRYNTQKLFSLNRYERTWNTSIIGSSVFGRRDIIYRKWK 903  
QY 692 TFVLRV-RAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIAIIPK--QNTYCVRRVAVVQ 748  
Db 904 EFVTKVFESGEMPHFYFVKGDVSRAFDTIPIHKLVESIVQVLKPESTQVYGIWVAVIM 963  
QY 749 KAAHGHVRKAFKSHVSTLTDLPYMRQFVAHLOETSPLDVAVVEOSSSLNEASSGLFDV 808  
Db 964 ITPTGKARKLYKRHVSTFEDFIPDMKQFVSKLQERTSLRNAIVVEQCLTFNENSTLTF 1023  
QY 809 FLREMFCHAVRJRGKSYVOCQIPQSGIILSTLLCSLCYGDMMENKLPAGIRRDGLLRLVD 868  
Db 1024 FLQMLHNLTLEGHRYIQCQSGIPQSGIILSTLLCSLCYGDMMENKLCGQKQGVLRLLD 1083  
QY 869 DFLVTPPHLTHAKTFLRTLVRGVPEYGVVNLKRTVVPFVEDEALGTFVQMPAHGLF 928  
Db 1084 DFLVTPHLMQARTLRTIAAGIPYGVFLINAKKTVVPFV-DDIPGCSKFHLPDCLRI 1142  
QY 929 PNCGLLDRTLEVSDSYSSYARTSIRASLTNRGFKAGNRMRKLVGVRLKCHSLFLD 988  
Db 1143 SMCGLLDVQTLLEVYCDYSSAFTSIRSSLSFNSRIAGKNNCKLTAVLKLKCHPLLD 1202  
QY 989 LQVNSLQVCTNIVYKILLQAVRFHACVLQLPFHQVWKNPTFFLRVSDTASLCYSILK 1048  
Db 1203 LKINSLOVVLINIKYIFLLQAVRFHACVLQFPNOKVRNPDFFLRISDTSACCYFLK 1262  
QY 1049 AKNAGMSLGAAGAAGPLPSEAVQWLCFOAFLLKLTTRHRTVTVPLIGSLRTAQOLSRKLP 1108  
Db 1263 AKNPGVSLGSDASGMFFPEAAEWLCYHAFIVKLSNKHVYKCLLKPLKYVMHLLFGKIP 1322  
QY 1109 GTTLTALAANAANPALPSDFKTLID 1132  
Db 1323 RDTMELLKTVPTEPSLCQDFKTLID 1346

## RESULT 10

QY 989 LQVNSLQVCTNIVYKILLQAVRFHACVLQLPFHQVWKNPTFFLRVSDTASLCYSILK 1048  
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RN NCBI_TaxID=8355;
RX SEQUENCE FROM N.A.
RP MEDLINE=21488334; PubMed=11602347;
RA Kuramoto M., Ohsumi K., Kishimoto T., Ishikawa F.;
RT "Identification and analysis of the Xenopus TERT gene that encodes the
RT catalytic subunit of telomerase.";
RL Gene 277:101-110(2001).
DR ENBL; AF212299; AAC7357.1; -.
DR CO; GO:0005634; C:nucleus; IEA.
DR CO; GO:0003677; C:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase.; IEA.
DR CO; GO:0016740; P:transferrase activity; IEA.
DR CO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000477; RTase.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT; 2.
DR PRINTS; PR01365; TELOMERASERT.
DR KW RNA-directed DNA polymerase; Transferrase.
SQ SEQUENCE 1191 AA; 138016 MW; 9BD9D776869A57D6 CRC64;

Query Match 38.9%; Score 2316.5; DB 2; Length 1191;
Best Local Similarity 42.4%; Pred. No. 4.9e-136;
Matches 518; Conservative 201; Mismatches 381; Indels 123; Gaps 25;

Qy 1 MPRAPCRVRSLLRSHYREVLPATFVRRLG-PQGNR--LVQRGDPAAPRALVAQCLVC 57
Db 1 MPRGTGATLLSILQRYGVGLVEYDTLQVPGGKVPVLLLEGDSKFRSFVAELVVC 60
Qy 58 VPMDDARPPAAPSPQVSCLEKELVARVLQRCERGAKNVLAFLGALLDARGGPPPEAFTT 117
Db 61 IPRTCKPLSPVSLQSTQREVVARVQICEKKNVLAFLGGLVD-EKSNLNLRLTP 119
Qy 118 SVRSYLPNTVTDALRGSGALLRRVGDVVLHLLARCALFVLVAPSCAYQVCGPLY- 176
Db 120 NICNYFNPPTTTISTISILWETLLTRVGDVVMYWLQCSIFVFPVPRCCYQITGPIYT 179
Qy 177 -----QLGANTQAR-----PPHASGPRRLGGERAWNHVRE 209
Db 180 LPSDDVLFQSQSTQSNVLLRYIKRVFHLRKKYLPKPGKSMTSRM-----LTWRRNKP 234
Qy 210 AGVPLGLPAPGARRGGASRSL-----PLPKRPRRGAPE-----PERTPVGGQ 254
Db 235 SGLLRKSTSWAVTETHSRKRLCKSDICVIPDKRRDNLKDDTVHFDLPMCRSVYL 294
Qy 255 SWAHPGR-----TRG-PSDRGFCVVSFAPPAEEATSLGALSGRH----- 294
Db 295 SNMYPKTNVQVGLITSGYKTKTFQCKQKVPSCQKKTAFYSVAGDNLSLKDNVNKLI 354
Qy 295 SHPSVGRQHAGPPSTSRPPWDTCPVVAETKFLY-SSGDKQLRPSFLLSSLRPS 353
Db 355 TNASV-----PTAQR-----LSFSNIPIDFGRTLYLSISYKGFSEFSLNLSDT 401
Qy 354 LTGARRLVETIFLGS-----RPMWPGTPRRLPQRYWQMRPLFLLGLGHACPY 405
Db 402 PSGQKLVETIFLNFLEAQNFQDKRDENCRY--KLPKRWKPKHPIQELIQHKKFPY 459
Qy 406 GVLLKTHCPURAAVTPAAGVCAREKPGQSGVAAPBEED-----TDPRLVQLLRQHS 457
Db 460 LVVLNKHCPVRSSM-----ACSEKR-----SLQKNRIENDGKQLKHTTKANLLSLKQHS 511
Qy 458 PWQYGFVRACLRRLVPPGLWNGSHRNERRFLNTKFISL-GKIAKLSLQELTWQMSVRD 516
Db 512 IWQYMFVRECLNNVDPDIMWGSHNKRFRFNKVSFLFTSGKFGKISLSLWMSMRVED 571
Qy 517 CAILRRSPGVCVPAASHRLREELTAKFLHLMVSVYVVELLSRSPFYVTTTFOKNRFFY 576
Db 572 CSWIRLQKSHFVPASEHLEKILAKFVFWLMDTYVQLLKSFPFYVTTTFQKRLFFY 631
Qy 577 KSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALITSRLRIFPKPDGLRPIVM 636
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Db 632 RKSVMKKLQNIQRLKHLKVKLSLSSELENMQQWKNVPLVSLRIPKTNGLRPTSKI 691
Qy 637 DYVVGARTER--REKRAERLTSRVKALFVSVLYNERARRPGLLGASVLGLDLDIHAWRTFV 694
Db 692 SSTLSQSQSKENQEKIHHFSSQIRNLFSVLNFWNRNCSLIGSVFGMDDIYKKNKKFV 751
Qy 695 LRV-RAQDPPELYFVKVDVTGAYDTIPQDRLTEVIAIIP--QNTYCVRRYAVVQKAA 751
Db 752 LDFEKPQVEKLQFVFKVTDVKGAYDTIPHSKLDDEVISKVINPNANEVYIRRYATVSDP 811
Qy 752 HGVKRAFKSHVSTLTLQPYMQQFVAHQETSLRDAVVIEQSSSNEASSGLFEDVPLR 811
Db 812 TGRIRKSKFRHVSLEADVLNPMKQFVSNQOEKLLRNLTLVEQNLNLSSESVKLLAVPQ 871
Qy 812 FMCHHVAIRIGKSVVOCQGIPOGSILSTLCSLCYGMENKLPAGIRRDGLLRLVDDFL 871
Db 872 IIRSHILIRIKORYMQCCGIPQGSMLSTILCSLCYGMENAMLGGIQNGVLMRLIDFL 931
Qy 872 LVTPHLTHAKTFLRLTVRGVPEYGCVVNLRKTVVNFVED--EALGGTAFVQMPAHGLFP 929
Db 932 LVTPHLDAQKTFRLTLAEGIPQYGCISIPQKTVVNFVDDIPEC---SEVEQLPSHCLFR 988
Qy 930 WCGLLDTRLEVSQDYSSYARTSIRASLTFNRGFKAGRNMRRLFGVLRKCHSLFLDL 989
Db 989 WCGLLDTRLEVSQDYSSYARTSIRASLTFNRGFKAGRNMRRLFGVLRKCHSLFLDL 1048
Qy 990 QVNSLQVTCNIVKILLQAVRPHACVLQLPFHQVWKNPTFFLRVSDTASLCVSLKA 1049
Db 1049 KVNLSRIVTCNTYKIFLQAYRHACVVQJPFQGVWNNPPFTLVISDMAPCYTTFFKA 1108
Qy 1050 KNAGMSLGAKGAAGPLPSEAVQWMLCHQAFLLKTLRHRVTYVPLGLSLRTAQLSRKLP 1109
Db 1109 KNKDLTRGYKDVSCQNFQVAVQWLSYQAFLLKLNHVKLYKCLIGPLQNCQWQLSRRLSQ 1168
Qy 1110 TTTTALAAANPALPSPDKTILD 1132
Db 1169 DTIELLSKSVTDSLLHKDFSCIMD 1191

RESULT 11
O94807 PRELIMINARY; PRT; 523 AA.
AC O94807;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Telomerase transcriptase (fragment).
GN Name=hTERT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99137484; PubMed=9973199;
RA Takakura M., Kyo S., Kanaya T., Hirano H., Takeda J., Yutsudo M.,
RA Inoue M.;
RT "Cloning of human telomerase catalytic subunit (hTERT) gene promoter
RT and identification of proximal core promoter sequences essential for
RT transcriptional activation in immortalized and cancer cells.";
RL Cancer Res. 59:551-557(1999).
DR ENBL; AB016767; BAA74724.1; -.
FR NON TER 523 523
SQ SEQUENCE 523 AA; 56555 MW; 8FDE562DDECC93DA CRC64;

Query Match 37.0%; Score 2207.5; DB 2; Length 523;
Best Local Similarity 78.7%; Pred. No. 1.1e-129;
Matches 435; Conservative 3; Mismatches 56; Indels 59; Gaps 6;

Qy 1 MPRAPCRVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAPRALVAQCLVCVPW 60
Db 1 MPRAPCRVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAPRALVAQCLVCVPW 60
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QY 61 DARPAPAPFQVSCIKELVARVLQRCERGAKNVLAFLGALLDARGGPPFAFTTSVR 120
DB 61 DARPAPAPFQVSCIKELVARVLQRCERGAKNVLAFLGALLDARGGPPFAFTTSVR 120
QY 121 SYLPTNTVDALRSGGANGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLVOLGA 180
DB 121 SYLPTNTVDALRSGGANGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLVOLGA 180
QY 181 ATQARPPPHASGRRRLRGCRANMHSVREAGVPLGLPAPGARRGGSSASRLPKPRR 240
DB 181 ATQARPPPHASGRRRLRGCRANMHSVREAGVPLGLPAPGARRGGSSASRLPKPRR 240
QY 241 GAAPEPERTVPGQSWAHGPRTRGSPDRGFCVSPARPABEATSLEGALSGTRHSPSVG 300
DB 241 GAAPEPERTVPGQSWAHGPRTRGSPDRGFCVSPARPABEATSLEGALSGTRHSPSVG 300
QY 301 ROHAGAPPTSRPRPMDTPCPVYATKHIFLYSSGDKQOLRPSFLSSLRPSLTGARRL 360
DB 301 ROHAGAPPTSRPRPMDTPCPVYATKHIFLYSSGDKQOLRPSFLSSLRPSLTGARRL 360
QY 361 VETIFLGSRPWPCPTPRRLPRLQRYWQMRPLFLELLGNHAQCPYGVLLKXTHCPLRAAVT 420
DB 361 VETIFLGSRPWPCPTPRRLPRLQRYWQMRPLFLELLGNHAQCPYGVLLKXTHCPLRAAVT 420
QY 421 PAAGVCAREKPPQSGAARPEBEDTPRRLVQLLRQHSPPQVYGFVRACLRLVPPGLW-- 478
DB 415 -----CELRSPQPPSVNP-----GRSPRAL-----W-----RPRRTQTPVAMCS 450
QY 479 -----GSRNERRFLRNTKXTISLGKHAQLSLQELTWK 511
DB 451 CSASTAPLAGVRLRAGLPAPAGAPRPLGLQARRRFLRNTKXTISLGKHAQLSLQELTWK 510
QY 512 MSVRDCAWLRSP 524
DB 511 MSVRDCAWLRSP 523
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RESULT 12

Q9JK99 PRELIMINARY; PRT; 575 AA.

AC Q9JK99; 15, Created

DT 01-OCT-2000 (TEmBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TEmBLrel. 25, Last annotation update)

DE Telomerase catalytic subunit (Fragment).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22860253; PubMed=13679242;

RA Wong S.C., Ong L.L., Er C.P., Gao S., Yu H., So J.B.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RT "Cloning of rat telomerase catalytic subunit functional domains,

RT reconstitution of telomerase activity and enzymatic profile of pig and

RT chicken tissues.";

RL Life Sci. 73:2749-2760(2003).

RN [2]

RP SEQUENCE FROM N.A.

RA Wong S., Gao S., Xu X., Yu H.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

EMBL; AF247818; AAF62177.1; -.

CO; GO:0005634; C:nucleus; IEA.

DR GO:0003677; F:DNA binding; IEA.

DR GO:0003723; F:RNA binding; IEA.

DR GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

DR GO:0003721; F:telomeric template RNA reverse transcripts. . .; IEA.

DR GO:0016740; F:transferase activity; IEA.

DR GO:0006278; P:RNA-dependent DNA replication; IEA.

DR InterPro; IPR004077; RVTse.

DR InterPro; IPR003545; Telomerase\_RT.

DR Pfam; PF00078; RVT; 1.

DR PRINTS; PR01365; TELOMERASERT.

KW RNA-directed DNA polymerase; Transferase.

FT NON\_TER 1

SQ SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;

Query Match 33.8%; Score 2016; DB 2; Length 575;

Best Local Similarity 67.6%; Pred. No. 1.2e-117;

Matches 391; Conservative 71; Mismatches 110; Indels 6; Gaps 3;

QY 558 RSFFYVTEFTQKRVLFYRKSVMSKLSQSTIGTIOHLKRVOLRSLSEAEVQREARALL 617

DB 1 RSFFYVTEFTQKRVLFYRKSVMSKLSQSTIGTIOHLKRVOLRSLSEAEVQREARALL 617

QY 618 TSLRLRIPKPDGLRPIVNNMDYVVGARTFRREKKAERLTSRVKALFSLVNYERARRPGLLG 677

DB 61 ICLRLRIPKPDGLRPIVNNMDYVVGARTFRREKKAERLTSRVKALFSLVNYERARRPGLLG 677

QY 678 ASVLGLDDIHRARWTRFVLVRADPPPELYFVKVDVTGAYDTTIPQRLTEVIAIITK-PQ 736

DB 121 SSVLGMNDIYRTWRAFLVRALDQTPRMVFKADVTGAYDAIPQGLVEVWAMIRHSE 180

QY 737 NTYCVRRYAVVOKAAHGHYRKAFKSHVSTLTDLQPYMRQFVAHLQET--SPLSDAVVIEQ 794

DB 181 STYCIHQYAVVRDSQGVHKSFRQVTTLSLDLPYMGQFLKHLQSDASALRNSVVEQ 240

QY 795 SSSLINEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSILSTLLCSLCYGDMMENKLF 854

DB 241 SISMNESSSLDFLFLRHSVVKIGDRCTYQCGIPQGSILSTLLCSLCYGDMMENKLF 300

QY 855 AGIRDGLLLRLVDDFLVTPHLLTHAKTFLRLVROGVPEYGVVNLKRTVNVFPVDEAL 914

DB 301 AEVQRDGLLRFDVDFLLVTPHLDQAKTFLSLVHGVPEYGCINLQKTWNFPVPGTL 360

QY 915 GGTAFVOMPAHGLFPWCGLLDTRTLEVSQSDYSSYARTSIRASLTNRGFKAGNRKRL 974

DB 361 GGAAPYQLPAHCLFPWCGLLDTRTLEVSQSDYSSYARTSIRASLTNRGFKAGNRKRL 420

QY 975 FGVRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVQLQFPHQOVKNPTFFLR 1034

DB 421 LSVRLKCHGLFDLDQVNSLQTVCTNIYKILLQAYRFHACVQLQFPHQOVKNPTFFLR 480

QY 1035 VISDTASLCYSILKAKNAGMSLGAAGAAGPLPSEAVQWLCHQAFLLKLTNRHRYVPLLG 1094

DB 481 IISQASCCVAILKVNKPGWTLKASG---FPPEAAHWCYQAFLLKLAHSAHVIYKCLLG 537

QY 1095 SLRTAQTLRKLPGLTTLTALEAANPALPSDEKTLID 1132

DB 538 PLRTAQTLRKLPGLTTLTALEAANPALPSDEKTLID 575

RESULT 13

Q9R266 PRELIMINARY; PRT; 514 AA.

ID Q9R266

AC Q9R266; 13, Created

DT 01-MAY-2000 (TEmBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TEmBLrel. 24, Last annotation update)

DE Telomerase reverse transcriptase (Fragment).

GN Name=Text;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99144726; PubMed=10022128;

RA Greenberg R.A., O'Hagan R.C., Deng H., Xiao Q., Hann S.R., Adams R.R.,

RA Lichtsteiner S., Chin L., Morin G.B., Depinho R.A.;

RT "Telomerase reverse transcriptase gene is a direct target of c-Myc but

RT is not functionally equivalent in cellular transformation.";

RL Oncogene 18:1219-1226(1999)

DR EMBL; AF121949; AAD24465.1; -.

DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

[illegible]

Db 687 FVADVFKAFSDVDQGLLHVIOFLKDE--YILNRCRLVCCGKRGNWNKILVSSDKNS 744  
QY 762 HVSTLTDLPYMRQFVAHLQETSLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVRIR 821  
Db 745 NFRFTSTVPYNA-----LQ-----SIVVDGENHRVRKKDLMVMWGNMKNMLQLD 792  
QY 822 GKSYVQCGIPQSGIISLTLCSLCYGDMEKLFAGI-----RRDGL----- 862  
Db 793 KSFVQIAGIPQGHRLSSLLCCFYGHLERTLIVPFLAEASKDVSSKECSREBELIPTS 852  
QY 863 --LLRLVDDPELLVPHLTHAKTFLRTLVRGPEYGCVVNLRKTVVNPFFVEDE----- 912  
Db 853 YKLLRFDDDLVSTSDQASSFVRLKHGFKDYNCFMNETKFCINPEDKEEHRCSNRM 912  
QY 913 --ALGGTAFQMPAHGLFPWCGLLDDRTLLEVQSDYSSYARTSIRASLTENRFKAGRM 970  
Db 913 FVGDGVPFVR-----WTGLINSRTFEVQVDYTRYLSGHSISSTFSVAMQNKVPRNL 964  
QY 971 RRLFGVRLRLKHSFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLPFFHQVWK-NP 1029  
Db 965 RQKLCYFLVPKCHPILPDSNINGSIEVRLNIYQIFLLAAMKFCYVVEV---SRFWKLHP 1021  
QY 1030 TFLRVISDTASLCYSILKAKNAGMSLGAK-GAAGPLPSEAVOWLCHQAPFLKLKTRHVT 1088  
Db 1022 QTLFKFTISVRYMFLINRRVRRINTGSSFRPVLKLYKEEVIMGLDVIQVLKKNR 1081  
QY 1089 YVPLGSLRTA-----QTOLSRKLPQTT 1111  
Db 1082 YRMLLIYKLSKLSQSLSELKYAT 1110

RESULT 15  
Q9SPU7 PRELIMINARY; PRT; 1123 AA.  
AC Q9SPU7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Telomerase reverse transcriptase.  
GN Name:ATERT; Synonyms:FSE19\_190;  
OS Arabidopsis thaliana (Mouset-ear cross).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99402974; PubMed=10471830;  
RA Oguchi K., Liu H., Tamura K., Takahashi H.;  
RT "Molecular cloning and characterization of AtTERT, a telomerase  
reverse transcriptase homolog in Arabidopsis thaliana.";  
RL FEBS Lett. 457:465-469 (1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,  
RA Tabata S., Mewes H.W., Ruid S., Lemcke K., Mayer K.F.X.;  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF135454; AAD54777.1; -;  
DR EMBL; AL391147; CAC01849.1; -;  
DR PIR; T51517; T51517;  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.  
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.  
DR InterPro; IPR000215; Prot\_inh\_serpin.  
DR InterPro; IPR000477; RVTse.

DR InterPro; IPR003545; Telomerase\_RT.  
DR Pfam; PF00078; RVT; 1.  
DR PRINTS; PRO1365; TELOMERASERT.  
DR PROSITE; PS00284; SERPIN, UNKNOWN 1.  
KW RNA-directed DNA polymerase; transferase.  
SQ SEQUENCE 1123 AA; 130579 MW; 5645B8295817B7F6 CRC64;  
  
Query Match 12.2%; Score 724.5; DB 2; Length 1123;  
Best Local Similarity 23.8%; Pred. No. 1.6e-36;  
Matches 294; Conservative 199; Mismatches 511; Indels 233; Gaps 39;  
  
QY 1 MPRAPCRRAVRSLRSHRYEVLPLATFV-----RRLGPGQWR-----L 38  
Db 1 MPKCPKRRHVRPEILWLFLGNRARNLNDIAI VDLIPNRNIQPCQCRGQGLGCGSSDKPAFL 60  
QY 39 VORGDPAAFRALVAQCLVCPWDARPPPAAPSPFRQVSCLELVARVQLRL---CERGAKN 95  
Db 61 LRSDDPIHYRKLHLRCFV-VLHEQTPPLDLDFTSWMQSOREIVERIEMMQSGCD--CON 117  
QY 96 VLAFGFALLDGAAGGPPPEAFTTSVRSYLPNTVTDALRGSGAWGLLRRVDDVVLHLLAR 155  
Db 118 VICARYDKYDQS-----SPLELLT-SSSWEFLKRVGHVDMVYLLQ 159  
QY 156 CALFVLVAPSCAYQCGPPLYQLGAAT-----QARPPPHASPRRRRLCGERAMNHSVR 209  
Db 160 TSIFLPLGKHKHQVSGPPLCIKHKRTLSVHENKGRDDNVQPTKROWLSSAVDDCPKD 219  
QY 210 AGVPLGLPAPG---ARRRGSASRSLPLPKPRGA-----APEPERTVPGGWSA 257  
Db 220 DSATI-TPIVGEDVDQHREKTKTSRIYLRKRRKQKYNFKKVDNACIITP----- 271  
QY 258 HPGRTGRPSDRGFCVVSPARPAEATSLGALSCTRHSHPSVGROHAGPPTSRPRPW 317  
Db 272 ---STNGKVSTG-----NDEMNLHIGINGSLTDFVKQAKQ----- 303  
QY 318 DTPCPVVAETKFLYS-SGDKEQLRPSFLSLSRPSLTGARRLVETIFLGRPMMPGT 376  
Db 304 -----VKNKNFKFGLSETYSVIPNHLKTLRPNCSKLLMNHIFGEVNVWSTTFS 356  
QY 377 RRLPLRPQ-----RYQMRLPFLLELGNHAQCPGYLLKTHCP-----LRAAVTAA 424  
Db 357 HOGKNCPSGICLYHSLKSLKXNLIGTKTSSHLKMLLDKPCVPLLQEDALSGTTSQS 416  
QY 425 VCAREK---PGGSVAA---PEEEDTDPRLVQLLRHSSPWQVYGFVACLRRLRVP 476  
Db 417 --RRQKADKLPHGSSSSGTGKPKCSVERKL-----YCTNDQVVSFWAICRYIVPS 468  
QY 477 LMGSRHNRRLNTKCFISLQGHAKLSQELTWKMSVRDCAWLRRSPGVCVPAAEHL 536  
Db 469 LLGTTQMRVLRKNIAWFVSRRRNEKCTVQFLHKVKPSDFPFARKE--LCCMVNGHEL 526  
QY 537 REE-----ILAFELHLMVSVYVVELLRSFPYVTEITTFQKNRLLFFYKSVMSKLQSIG 588  
Db 527 QSESIRSTQMLCTKWISWLFLEIVKLVHFNFYATESQGGRLNIYYIKRSWERLISKE 586  
QY 589 IRQHLKRVOLRELSAEVROHREARPAULTSLRFLPKPDGLRPIVMYVVGARFRRE 648  
Db 587 ISKALDGYLVDDAEBSRKK-----LSRFLPKANGVRWLD-----FSSS 630  
QY 649 KRAERLTSRKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVADQPP-PELY 707  
Db 631 SRSSQL---RDTHAVLKDIQLKPEDVLGSSVDFDHFYRNLCPLYLHLRSQSGELPLY 686  
QY 708 FVKVDVTGAYDTIPQDRLTEVIASIKPQNTYCVRYAVYQAAHCH-----VRKAFKS 761  
Db 687 FVADVFKAFSDVDQGLLHVIOFLKDE--YILNRCRLVCCGKRGNWNKILVSSDKNS 744  
QY 762 HVSTLTDLPYMRQFVAHLQETSLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVRIR 821  
Db 745 NFRFTSTVPYNA-----LQ-----SIVVDGENHRVRKKDLMVMWGNMKNMLQLD 792  
QY 822 GKSYVQCGIPQSGIISLTLCSLCYGDMEKLFAGI-----RRDGL----- 862

Db	793	KSFVQIAGIPQGHRLSSLLCCFYVYGHLERTLIIYPFLEEASKOVSSKECSREBELIIPTS	852
Qy	863	--LLRLVDDFLLVTPHLLTHAKTFLTLVRGVPEYGCYVNLKTKTVNFPFVEDE-----	912
Db	853	YKLLRFDDYLFVSTSRDQASSFYHRLKHGFKDYNCFMNETKFCINFEDKEEHRCSSNRM	912
Qy	913	--ALGGTAFVQMPAHGLFPWCGLLDTRTLEVOQSDYSSYARTSIRASLTFRNGFKAGRNM	970
Db	913	FVGDNQVFPFVR-----WTGLLINSRTFEVQVDYTRYLSGHISSSTFSVAWQNKPVRL	964
Qy	971	RRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLPHEHQOVWK-NP	1029
Db	965	RQKLCYFLVPKCHPILFDSNINSGEIVRLNIYQIFLLAAMKPHCYVYEV---SRFWKLHP	1021
Qy	1030	TFFLRVISDTASLCYSILKAKNAGMSLGAK-GAAGPLPSEAVOWLCHQAFLLKLTRHRVT	1088
Db	1022	QTLFKFITISVRVYMERLINRVRINTGSSFRPVLYKEEVIWGLDVIQVLKKNSR	1081
Qy	1089	YVPLLGSIRTAQTO--LSRKLPGTTLTALEAAANPAL	1123
Db	1082	YRMLLIYKLSALSKHLSQLSSELRYATDRSNSSSL	1118

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OM protein - protein search, using sw model

Run on: January 10, 2005, 17:32:00 ; Search time 42 Seconds  
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1787.428 Million cell updates/sec

Title: US-10-053-758-225

Perfect score: 5961  
Sequence: 1 MPRAPRCRAVRLRLSHYRE.....TALEAANPALPSDFKTILD 1132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_patents\_AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5961	100.0	1132	3	US-08-851-843A-225
2	5961	100.0	1132	3	US-08-974-549A-2
3	5961	100.0	1132	3	US-08-851-843A-225
4	5961	100.0	1132	3	US-08-974-549A-2
5	5961	100.0	1132	3	US-08-851-843A-225
6	5961	100.0	1132	4	US-08-974-549A-2
7	5961	100.0	1132	4	US-08-851-843A-225
8	5961	100.0	1132	4	US-08-974-549A-2
9	5961	100.0	1132	4	US-08-851-843A-225
10	5961	100.0	1132	4	US-08-974-549A-2
11	5961	100.0	1132	4	US-08-851-843A-225
12	5961	100.0	1132	4	US-08-974-549A-2
13	5961	100.0	1154	3	US-08-974-549A-611
14	5961	100.0	1154	4	US-08-974-549A-611
15	5961	100.0	1154	4	US-08-974-549A-611
16	5961	100.0	1154	4	US-08-974-549A-611
17	5961	100.0	1189	3	US-08-974-549A-613
18	5961	100.0	1189	4	US-08-974-549A-613
19	5961	100.0	1189	4	US-08-974-549A-613
20	5961	100.0	1189	4	US-08-974-549A-613
21	5961	100.0	1200	3	US-08-974-549A-612
22	5961	100.0	1200	4	US-08-974-549A-612
23	5961	100.0	1200	4	US-08-974-549A-612
24	5961	100.0	1200	4	US-08-974-549A-612
25	5961	100.0	1285	3	US-08-974-549A-600
26	5961	100.0	1285	4	US-08-974-549A-600
27	5961	100.0	1285	4	US-08-974-549A-600

Sequence 600, App  
Sequence 344, App  
Sequence 344, App  
Sequence 344, App  
Sequence 628, App  
Sequence 334, App  
Sequence 628, App  
Sequence 628, App  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 217, App  
Sequence 336, App  
Sequence 217, App  
Sequence 217, App  
Sequence 217, App  
Sequence 336, App  
Sequence 336, App

## ALIGNMENTS

RESULT 1  
US-08-851-843A-225  
; Sequence 225, Application US/08851843A  
; Patent No. 6093809

### GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Hartley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. 6093809el Telomerase  
NUMBER OF SEQUENCES: 225

### CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

### COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,843A  
FILING DATE: 06-MAY-1997  
CLASSIFICATION:

### PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION:

### PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION:

### PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION:

### ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 225:

330/123

08

08/676967

SEQUENCE CHARACTERISTICS:  
LENGTH: 1132 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-851-843A-225

Query Match 100.0%; Score 5961; DB 3; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPLATEFVRLPGQWRLVQGDPAAFRALVAQCLVCVPW 60  
Db 1 MPRAPRCRAVRSLLRSHYREVLPLATEFVRLPGQWRLVQGDPAAFRALVAQCLVCVPW 60  
Qy 61 DARRPPAPSPROVSCIKELVARVLQRLCERGAQNVLAFCFALLDARGGPPFAFTTSVR 120  
Db 61 DARRPPAPSPROVSCIKELVARVLQRLCERGAQNVLAFCFALLDARGGPPFAFTTSVR 120  
Qy 121 SYLPTNTVDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLVOLGA 180  
Db 121 SYLPTNTVDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLVOLGA 180  
Qy 181 ATQARPPHAGSPRRRLGCBRAWNHSVREAGVPLGPAAGARRRGGSASRSLPLPKRPRR 240  
Db 181 ATQARPPHAGSPRRRLGCBRAWNHSVREAGVPLGPAAGARRRGGSASRSLPLPKRPRR 240  
Qy 241 GAAPEPERTVVGOGSWAHPCGTRGSDRGFCVVSPPARPAEATSLGALSGTTHSHPSVG 300  
Db 241 GAAPEPERTVVGOGSWAHPCGTRGSDRGFCVVSPPARPAEATSLGALSGTTHSHPSVG 300  
Qy 301 RQHAGPPSTSRPRPMDTPCPPVYAEKHFLLYSSGDKQOLRPSFLLSSLRPSLTGARRL 360  
Db 301 RQHAGPPSTSRPRPMDTPCPPVYAEKHFLLYSSGDKQOLRPSFLLSSLRPSLTGARRL 360  
Qy 361 VETIFGSRPWPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420  
Db 361 VETIFGSRPWPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420  
Qy 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRQHSPPWQYGFVRACLRLVPPGLWS 480  
Db 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRQHSPPWQYGFVRACLRLVPPGLWS 480  
Qy 481 RHNERRFLNTKKFISLGKHAQLSLOELTWKMSVRDCAMLRSPGVGCVPAAEHRLREEI 540  
Db 481 RHNERRFLNTKKFISLGKHAQLSLOELTWKMSVRDCAMLRSPGVGCVPAAEHRLREEI 540  
Qy 541 LAKFLHLMMSVYVVELLRSFFYVTTTFOKNRLFYRKSVWSKLQSIGIRQHLKRVOLRE 600  
Db 541 LAKFLHLMMSVYVVELLRSFFYVTTTFOKNRLFYRKSVWSKLQSIGIRQHLKRVOLRE 600  
Qy 601 LSAEVRQHREARPAALLTSRLREIPKPDGLRPIVNMNDYVVGARTFRREKRAELTSTRKA 660  
Db 601 LSAEVRQHREARPAALLTSRLREIPKPDGLRPIVNMNDYVVGARTFRREKRAELTSTRKA 660  
Qy 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720  
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720  
Qy 721 PQRLTEVIASIIKPQNTYCVRYAVVQKAAGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780  
Db 721 PQRLTEVIASIIKPQNTYCVRYAVVQKAAGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780  
Qy 781 QETSPLRDADVIVQSSSLNEASSGLFDVFLRFCHHAVRIRGKSVYQCQGIPOGSTLSLTL 840  
Db 781 QETSPLRDADVIVQSSSLNEASSGLFDVFLRFCHHAVRIRGKSVYQCQGIPOGSTLSLTL 840  
Qy 841 LCSLCYGDMEKLFAGIRRDGLLRLVDDPFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900  
Db 841 LCSLCYGDMEKLFAGIRRDGLLRLVDDPFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900  
Qy 901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSYVARTSIRASLTF 960  
Db 901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSYVARTSIRASLTF 960

RESULT 2

US-08-974-549A-2  
; Sequence 2, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harlev, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:



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/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph Ted
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1132 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-974-549A-2

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Query Match	100.0%;	Score 5961;	DB 3;	Length 1132;
Best Local Similarity	100.0%;	Prod. No. 0;		
Matches 1132;	Conservative	0;	Mismatches	0;
			Indels	Gaps
			0;	0;
Qy	1	MPRAPRCRAVRSLLRSHRYEVLPLATFVRRLPGOGWRLVQRGDPAAPRALVAQCLVCVPW	60	
Db	1	MPRAPRCRAVRSLLRSHRYEVLPLATFVRRLPGOGWRLVQRGDPAAPRALVAQCLVCVPW	60	
Qy	61	DARPPPAAPSFQVSCSLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAFTTSVR	120	
Db	61	DARPPPAAPSFQVSCSLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAFTTSVR	120	
Qy	121	SYLPNTVTDALRSGGANGLLRRVGGDVLVHLLARCALFVLVAWSCAYQVCGPPLYQLGA	180	
Db	121	SYLPNTVTDALRSGGANGLLRRVGGDVLVHLLARCALFVLVAWSCAYQVCGPPLYQLGA	180	
Qy	181	ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLPKPRR	240	
Db	181	ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLPKPRR	240	
Qy	241	GAAPEPERTVPGQSWAHPGKTRGSPDRGFCVWSPARPAEATSLEGALSGTRSHSPVG	300	
Db	241	GAAPEPERTVPGQSWAHPGKTRGSPDRGFCVWSPARPAEATSLEGALSGTRSHSPVG	300	
Qy	301	RQHAGPPTSRSRPPRWDTCPPVYATKHPLYSSGDKQQLRPSFLSSLRPSLTGARRL	360	
Db	301	RQHAGPPTSRSRPPRWDTCPPVYATKHPLYSSGDKQQLRPSFLSSLRPSLTGARRL	360	
Qy	361	VEITFLGSRPWPMPCTPRRLPRLPORVQWMPRLFLELLGNHAQCYPGYVLLKTHCPLEAAVT	420	
Db	361	VEITFLGSRPWPMPCTPRRLPRLPORVQWMPRLFLELLGNHAQCYPGYVLLKTHCPLEAAVT	420	
Qy	421	PAAGVCAREKPOGSVAAPEBEDTDRRLVQLLRHSSPQWYGVFVRACLRRLVPPGLWGS	480	
Db	421	PAAGVCAREKPOGSVAAPEBEDTDRRLVQLLRHSSPQWYGVFVRACLRRLVPPGLWGS	480	
Qy	481	RHNERRLRNTKXFI SLGKHAKLSLQELTWKMSVRDCAWLRSSPGVGCVPAAEHLRREI	540	
Db	481	RHNERRLRNTKXFI SLGKHAKLSLQELTWKMSVRDCAWLRSSPGVGCVPAAEHLRREI	540	
Qy	541	LAKPLHLWMSVYVVELLRSFFYVTTTFQKNRLFYFKSVMSLQSIGIRQHLKRVQLE	600	
Db	541	LAKPLHLWMSVYVVELLRSFFYVTTTFQKNRLFYFKSVMSLQSIGIRQHLKRVQLE	600	
Qy	601	LSAEVROHREARPALITSRLRFTPKDGLRPIVNMDYVVGARTFREKRAERLTSRVKA	660	
Db	601	LSAEVROHREARPALITSRLRFTPKDGLRPIVNMDYVVGARTFREKRAERLTSRVKA	660	
Qy	661	LFSVLNYERARRPGLLGASVLGLDDIHRAWTTFVLVRQAQPPPELYFVKVDVDTGAYDTI	720	
Db	661	LFSVLNYERARRPGLLGASVLGLDDIHRAWTTFVLVRQAQPPPELYFVKVDVDTGAYDTI	720	
Qy	721	QDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGVKAFKSHSVSTLTDLQYMRQFVAHL	780	
Db	721	QDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGVKAFKSHSVSTLTDLQYMRQFVAHL	780	

RESULT 3  
US-08-854-050-225  
; Sequence 225, Application US/08854050  
; Patent No. 6261836  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6261836el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.

```

; ; REGISTRATION NUMBER: 36,429
; ; REFERENCE/DOCKET NUMBER: 015389-0029300US
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: (415) 576-0200
; ; TELEFAX: (415) 576-0300
; ; INFORMATION FOR SEQ ID NO: 225:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 1132 amino acids
; ; TYPE: amino acid
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
US-08-854-050-225

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Query Match	100.0%;	Score 5961;	DB 3;	Length 1132;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLGPGCWLVRGDDPAAFRALVAOCLVCVPW	60
DB	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLGPGCWLVRGDDPAAFRALVAOCLVCVPW	60
QY	61	DARPPPAAPFRQVSCULKEIVARVLQRLCBGAKNVIAFGFALLDGARGPPEAFTTSVR	120	
DB	61	DARPPPAAPFRQVSCULKEIVARVLQRLCBGAKNVIAFGFALLDGARGPPEAFTTSVR	120	
QY	121	SYLPNTVTDALRSGAGWLLLRVGGDVLVHLLARCALFVLVAPSCAYVCGGPLYOLGA	180	
DB	121	SYLPNTVTDALRSGAGWLLLRVGGDVLVHLLARCALFVLVAPSCAYVCGGPLYOLGA	180	
QY	181	ATOARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKPRR	240	
DB	181	ATOARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKPRR	240	
QY	241	GAPEPERTVPGGSAWHPGRTGPSDRGFCVVSPPAPAEATNSLEGALSGTRHSHPSVG	300	
DB	241	GAPEPERTVPGGSAWHPGRTGPSDRGFCVVSPPAPAEATNSLEGALSGTRHSHPSVG	300	
QY	301	RQHAGPPPTSRPRPMDTCPVPAETHKFLYSSGDKEOQLRSFLLSSLRPSLTGARRL	360	
DB	301	RQHAGPPPTSRPRPMDTCPVPAETHKFLYSSGDKEOQLRSFLLSSLRPSLTGARRL	360	
QY	361	VETIFLGSRPWPGTFRRLPRLPQRYQWMPRLFLELGNHAQCPYGVLLKTHCPLRAAVT	420	
DB	361	VETIFLGSRPWPGTFRRLPRLPQRYQWMPRLFLELGNHAQCPYGVLLKTHCPLRAAVT	420	
QY	421	PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLRQHSPPQWYGVFVRACLRRLVPPGLWGS	480	
DB	421	PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLRQHSPPQWYGVFVRACLRRLVPPGLWGS	480	
QY	481	RINERRFLNKTTFISLGKHAKLSQELTWKMSVRDCAMLRSPGVCYPAAEHLRREEI	540	
DB	481	RINERRFLNKTTFISLGKHAKLSQELTWKMSVRDCAMLRSPGVCYPAAEHLRREEI	540	
QY	541	LAKFLHLMMSVYVELLRSPFYVTTTFQKNRLFYFRKWSWKLQSIGIRQHILRVQLRE	600	
DB	541	LAKFLHLMMSVYVELLRSPFYVTTTFQKNRLFYFRKWSWKLQSIGIRQHILRVQLRE	600	
QY	601	LSEAEVRQREARPALLTSRLRFIPKPDGLRPTVNMDDYVVGARTFRREKRAERLTSRVKA	660	
DB	601	LSEAEVRQREARPALLTSRLRFIPKPDGLRPTVNMDDYVVGARTFRREKRAERLTSRVKA	660	
QY	661	LFSVLNYERARRPGLLGASVILGDDTHRAWRFTVLVRADQDPPPELYFVKVDVTGAYDTI	720	
DB	661	LFSVLNYERARRPGLLGASVILGDDTHRAWRFTVLVRADQDPPPELYFVKVDVTGAYDTI	720	
QY	721	PODRLTEVIASIIKPNQTYCVRRYAVVQKAAGHGVKAFKSHVSTLTDLPQYMRQFVAHL	780	
DB	721	PODRLTEVIASIIKPNQTYCVRRYAVVQKAAGHGVKAFKSHVSTLTDLPQYMRQFVAHL	780	
QY	781	QETSPLRDVAVIEQSSSLNEASGLPDVFLRFMCHHAVIRKGSYVQCQGIPOGSIILSTL	840	
DB	781	QETSPLRDVAVIEQSSSLNEASGLPDVFLRFMCHHAVIRKGSYVQCQGIPOGSIILSTL	840	

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; TOPOLOGY: linear									
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Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPGQWRLVORGDDPAAAFRALVAQCLVCVPW	60						
Qy	61	DARPPPAAPSPROVSCSKELVARVLQRLCERGAKNVLAFAFGALLDARGGPEAFTTSVR	120						
Db	61	DARPPPAAPSPROVSCSKELVARVLQRLCERGAKNVLAFAFGALLDARGGPEAFTTSVR	120						
Qy	121	SYLPNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPLYQLGA	180						
Db	121	SYLPNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPLYQLGA	180						
Qy	181	ATOARPPPHASGPRRLRGGERAWNHSVREAGVPLGLPAGARRGGSGASRSLPLPKPRR	240						
Db	181	ATOARPPPHASGPRRLRGGERAWNHSVREAGVPLGLPAGARRGGSGASRSLPLPKPRR	240						
Qy	241	GAAPERTPVGQGSWAHPGRTGRGSDRGFCVVSPPARPAEATSLEGALSGTRHSHPSVG	300						
Db	241	GAAPERTPVGQGSWAHPGRTGRGSDRGFCVVSPPARPAEATSLEGALSGTRHSHPSVG	300						
Qy	301	ROHAGPPSTSRPPMDTPCPVYAEKHLFYSGGDEQQLRPSLSLSPSTTGARRL	360						
Db	301	ROHAGPPSTSRPPMDTPCPVYAEKHLFYSGGDEQQLRPSLSLSPSTTGARRL	360						
Qy	361	VETIFLGSRPWPGTTPRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPLEAAVT	420						
Db	361	VETIFLGSRPWPGTTPRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPLEAAVT	420						
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Db	481	RHNERFLRNTKFIISLGKHAKLISLOELTWKMSVRDCNWLRRSPGVCVPAAEHRLREEI	540						
Qy	541	LAKELHMLMSYVVVELLSRFFVTTTFQKNRLFYRKSVMKLSQSIGIROLKRVOLRE	600						
Db	541	LAKELHMLMSYVVVELLSRFFVTTTFQKNRLFYRKSVMKLSQSIGIROLKRVOLRE	600						
Qy	601	LSEAEVRQHRARPALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA	660						
Db	601	LSEAEVRQHRARPALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA	660						
Qy	661	LFSVLNTERARRPGLGASVLGLDDIHRAMWTFVLVRAQDPPPELYFVKVDVTGAYDTI	720						
Db	661	LFSVLNTERARRPGLGASVLGLDDIHRAMWTFVLVRAQDPPPELYFVKVDVTGAYDTI	720						
Qy	721	PODLRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMQFVAHL	780						
Db	721	PODLRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMQFVAHL	780						
Qy	781	QETSPLRDVAVIEQSSLINEASSGLFDVFLRFMCHAVRIRGKSYVOCQIPQGSII STL	840						
Db	781	QETSPLRDVAVIEQSSLINEASSGLFDVFLRFMCHAVRIRGKSYVOCQIPQGSII STL	840						
Qy	841	LCSLCYGDMENKLFAGIRRDGLLRLVDDFLVLTPLTHAKTFLRTLVRGVPEYGCVVNL	900						
Db	841	LCSLCYGDMENKLFAGIRRDGLLRLVDDFLVLTPLTHAKTFLRTLVRGVPEYGCVVNL	900						
Qy	901	RKTVNFPVEALGGTAFVQMPAHGLFPWCGLLDDTTLTLEVDQSDYSYARTSTRSLTF	960						
Db	901	RKTVNFPVEALGGTAFVQMPAHGLFPWCGLLDDTTLTLEVDQSDYSYARTSTRSLTF	960						
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; Sequence 2, Application US/09128354									
; Patent No. 6337200									
; GENERAL INFORMATION:									
; APPLICANT: Morin, Gregg B.									
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants									
; FILE REFERENCE: 015389-003310US									
; CURRENT APPLICATION NUMBER: US/09/128,354									
; CURRENT FILING DATE: 1998-08-03									
; EARLIER APPLICATION NUMBER: US 08/851,843									
; EARLIER FILING DATE: 1997-05-06									
; EARLIER APPLICATION NUMBER: US 08/854,050									
; EARLIER FILING DATE: 1997-05-09									
; EARLIER APPLICATION NUMBER: US 08/911,312									
; EARLIER FILING DATE: 1997-08-14									
; EARLIER APPLICATION NUMBER: US 08/912,951									
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; EARLIER APPLICATION NUMBER: US 08/915,503									
; EARLIER FILING DATE: 1997-08-14									
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618									
; EARLIER FILING DATE: 1997-10-01									
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885									
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; EARLIER APPLICATION NUMBER: US 08/974,549									
; EARLIER FILING DATE: 1997-11-19									
; EARLIER APPLICATION NUMBER: US 08/974,584									
; EARLIER FILING DATE: 1997-11-19									
; EARLIER APPLICATION NUMBER: US 09/052,864									
; EARLIER FILING DATE: 1998-03-31									
; NUMBER OF SEQ ID NOS: 21									
; SOFTWARE: PatentIn Ver. 2.0									
; SEQ ID NO 2									
; TYPE: PRT									
; LENGTH: 1132									
; ORGANISM: Homo sapiens									
US-09-128-354-2									
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Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPGQWRLVORGDDPAAAFRALVAQCLVCVPW	60						
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Qy	61	DARPPPAAPSPROVSCSKELVARVLQRLCERGAKNVLAFAFGALLDARGGPEAFTTSVR	120						
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Qy	121	SYLPNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPLYQLGA	180						
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Qy	181	ATOARPPPHASGPRRLRGGERAWNHSVREAGVPLGLPAGARRGGSGASRSLPLPKPRR	240						
Db	181	ATOARPPPHASGPRRLRGGERAWNHSVREAGVPLGLPAGARRGGSGASRSLPLPKPRR	240						
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Db 241 GAAPEPRTVQGSWAHPGRTRGSPDRGFCVVSPPARPAEBATSLEGALSGTRHSPSVG 300  
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RESULT 6  
US-09-675-321-2  
; Sequence 2, Application US/09675321  
; Patent No. 6440735  
; GENERAL INFORMATION:  
; APPLICANT: Gaeta, Federico C.A.  
; APPLICANT: Geron Corporation  
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune  
; FILE OF INVENTION: Response to a Telomerase Antigen  
; FILE REFERENCE: 015389-003500PC  
; CURRENT APPLICATION NUMBER: US/09/675,321  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/112,006

; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
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; LENGTH: 1132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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RESULT 7  
US-09-052-919-2  
; Sequence 2, Application US/09052919  
; Patent No. 644650  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Antisense Compositions for Detecting and  
; TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/052,919  
; FILING DATE: 31-MAR-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/974,549  
; FILING DATE: 19-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/974,584  
; FILING DATE: 19-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17895  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parent, Annette S.  
; REGISTRATION NUMBER: 42,058  
; REFERENCE/DOCKET NUMBER: 015389-003600US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1132 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-052-919-2  
  
Query Match 100.0%; Score 5961; DB 4; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRLPGQWELVORGDPAAFRALVAQCLVCVPM 60  
  
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Db 61 DARPPPAAPFRQVSCIKELVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120  
  
Qy 121 SYLPTNTVDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPLYLQGA 180  
Db 121 SYLPTNTVDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPLYLQGA 180  
  
Qy 181 ATQARPPPHASGPRRLGCRANVHVSREAGVPLGLPAGARRRRGGSASRSLPLPKPRR 240  
Db 181 ATQARPPPHASGPRRLGCRANVHVSREAGVPLGLPAGARRRRGGSASRSLPLPKPRR 240  
  
Qy 241 GAAPEPERTVPGQSWAHPCGTRGSDRGFCVVSPPARPEATSLEGALSGTRHSHPSVG 300  
Db 241 GAAPEPERTVPGQSWAHPCGTRGSDRGFCVVSPPARPEATSLEGALSGTRHSHPSVG 300  
  
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Db 301 RQHHAGPSTSRPPRPWDTCPPVYAEKHLFVSSGDKQLRPSFLSSLRPSLTGARRL 360  
  
Qy 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELGNHAQCQYGVLLKTHCPFLRAVT 420  
Db 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELGNHAQCQYGVLLKTHCPFLRAVT 420  
  
Qy 421 PAAGVCAREKPOGQSVAAPEEEDTDPRRLVOLLRQHSPPQWYGVFVRACLRLVPPGLWGS 480  
Db 421 PAAGVCAREKPOGQSVAAPEEEDTDPRRLVOLLRQHSPPQWYGVFVRACLRLVPPGLWGS 480  
  
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Db 481 RHNERFLRNTKKFISLGKIAKLSLOELTWKMSVDCAWLRRSPGVCGVPAAEHRLREEI 540  
  
Qy 541 LAKFLHLMWSVYVVELLRSFFYVTTTFOKNLFFYFKSVKLSQSIGIRQHLKRVOLRE 600  
Db 541 LAKFLHLMWSVYVVELLRSFFYVTTTFOKNLFFYFKSVKLSQSIGIRQHLKRVOLRE 600  
  
Qy 601 LSEAEVQRHREARPALTLRLRFLPKDGLRPIVNDYVVGARTFRREKRAERLTSRYKA 660

Db 601 LSEAEVQHQREARPAALLTSRLRFPKPDGLRPIVNDVYVGARTFRREKGAERLTSRVA 660  
QY 661 LFSVLNVERARPPGLIGASVLGDDIHRAWRTFVLVRADQPPBELYFKVDVTGAYDTI 720  
Db 661 LFSVLNVERARPPGLIGASVLGDDIHRAWRTFVLVRADQPPBELYFKVDVTGAYDTI 720  
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Db 721 PDRLTEVIASIIKQNTYCVARYAVVQAAHGHVRKAFKSHVSTLTDLPVMOQFVAHL 780  
QY 781 QTSPLRDVAVTEQSSSNEASSGLFDVFLRPMCHAVRIRGKSVVQCQIGPOQSII STL 840  
Db 781 QTSPLRDVAVTEQSSSNEASSGLFDVFLRPMCHAVRIRGKSVVQCQIGPOQSII STL 840  
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Db 841 LCSLCYGDMMENKLFAGIRRDGLLRVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900  
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Db 901 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVQSDYSYARTSIRASLTF 960  
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Db 961 NRGFKAGNMRRKLFVLRKCHSLFLLQVNSLQTVCTNIYKILLQAYRFHACVQLQP 1020  
QY 1021 FHQQWKNPTFFLRVISDASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080  
Db 1021 FHQQWKNPTFFLRVISDASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080  
QY 1081 KLTRHRTVYVPLGSLRTAQOLSKRLPGTTLTAAEAANPALPSPDKTILD 1132  
Db 1081 KLTRHRTVYVPLGSLRTAQOLSKRLPGTTLTAAEAANPALPSPDKTILD 1132

## RESULT 8

US-08-912-951-2  
; Sequence 2, Application US/08912951  
; Patent No. 6475789  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
; THERAPEUTIC METHODS  
; NUMBER OF SEQUENCES: 335  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,951  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002600US  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1132 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-912-951-2  
Query Match 100.0%; Score 5961; DB 4; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPOQWRLVQRGDPAAPRALVAQCILVCVPM 60  
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Db 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGAPGARRRGGSASRSLPLPKPRR 240  
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Db 241 GAAPEPRTVPGQSWAHGRTGPGDRGFCVVSPPARPAEATSLGALSSTRHSHPVS 300  
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Db 481 RHNERFLRNTKKFISLGKHAHLSLQELTWKMSVRDCAMLRSPGVCVPAAEHRLREEI 540  
QY 541 LAKFLHMLMSVYVVELLSRFYVTTTFOKNRLLFFYRKSVWSKLQIGIRHKLKVOLRE 600  
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Db 601 LSEAEVROHREARPAALLTSRLRFTPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRVKA 660  
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Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWKTFVLVRQAODPPPELYFVKVDVTGAYDTI 720  
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RESULT 9

US-09-402-181B-2  
; Sequence 2, Application US/09402181B  
; Patent No. 6610839  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 633  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/402,181B  
; FILING DATE: 29-Sep-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ausehus, Scott L.  
; REGISTRATION NUMBER: 42,271  
; REFERENCE/DOCKET NUMBER: 015389-002620US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1132 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-402-181B-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 541 LAKFLHLMMSVYVVELLRSFFYTETFOKNRLLFFYRKSVWSKLQSIGIRQHLKRVOLRE 600

QY 601 LSEAEVROHREARPAALLTSRLRFTPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 660  
Db 601 LSEAEVROHREARPAALLTSRLRFTPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 660  
QY 661 LFSVLNVERARRPGLGASVLGLDDIHRAMRTFVLVRADQPPPELYFVKVDVTGAYDTI 720  
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QY 781 QETSPLRDVAVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOQSILSTL 840  
Db 781 QETSPLRDVAVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOQSILSTL 840  
QY 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLLVTPHILTHAKTFILTRIVRGVPEYGCVVNL 900  
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Db 1081 KLTRHRTVYVPLGLSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTLTD 1132

RESULT 10

US-09-721-456-2  
; Sequence 2, Application US/09721456  
; Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-NOV-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
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; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1132 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-721-456-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPCRRAVRSLLRSHYREVLPATFVRRLGPOGWRVQVGDPAAFRALVAQCLVCVPM 60  
Db 1 MPRAPCRRAVRSLLRSHYREVLPATFVRRLGPOGWRVQVGDPAAFRALVAQCLVCVPM 60  
QY 61 DARPPAAPSPFQVSKLKVLRVQLRCERCAKVNLAFFGALLDGAAGPPEAFTTSVR 120  
Db 61 DARPPAAPSPFQVSKLKVLRVQLRCERCAKVNLAFFGALLDGAAGPPEAFTTSVR 120  
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYVCGPPLYQLGA 180  
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYVCGPPLYQLGA 180  
QY 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRGGSASRSPLPKRPRR 240  
Db 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRGGSASRSPLPKRPRR 240  
QY 241 GAAPEPRTFVQGSWAHPGRTGRPSDRGFCVVSAPAEAEATSLEGALSGRTRHSHPSVG 300  
Db 241 GAAPEPRTFVQGSWAHPGRTGRPSDRGFCVVSAPAEAEATSLEGALSGRTRHSHPSVG 300  
QY 301 RQHAGPSTSRPPRPWDTPCPVVAETKHFYSSGDKQLRPSFLLSSLRPSLTGARRL 360  
Db 301 RQHAGPSTSRPPRPWDTPCPVVAETKHFYSSGDKQLRPSFLLSSLRPSLTGARRL 360  
QY 361 VETIFLGSRPWMPGTFRRLPRLPQRYQWVRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420  
Db 361 VETIFLGSRPWMPGTFRRLPRLPQRYQWVRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420  
QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSEPMQVYGFVRACLRLRVPGLMGS 480  
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSEPMQVYGFVRACLRLRVPGLMGS 480  
QY 481 RHNERFLRNTKKFISLQKHAKLSLOELTWKSVRDCAWLRSPGCVGCPVPAEHLRBEI 540  
Db 481 RHNERFLRNTKKFISLQKHAKLSLOELTWKSVRDCAWLRSPGCVGCPVPAEHLRBEI 540



Qy 541 LAKFLHLMMSVYVVELLRSFFYVTTTQKRLRPFYKSVNSKLSQSGIROHLKRVQIRE 600  
Db 541 LAKFLHLMMSVYVVELLRSFFYVTTTQKRLRPFYKSVNSKLSQSGIROHLKRVQIRE 600  
Qy 601 LSEAEVRHREARPAALLTSRLRFIPKPDGLRPIVNMDEVVVGARTFREKRAERLTSRVKA 660  
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Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLRAQDPPPELYFKVDVDTGAYDTI 720  
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLRAQDPPPELYFKVDVDTGAYDTI 720  
Qy 721 PQDLRTEVIASIIKPONTYCVRRYAVVQAAHGHVRKAFKSHVSTLTLQPYMRQFVAHL 780  
Db 721 PQDLRTEVIASIIKPONTYCVRRYAVVQAAHGHVRKAFKSHVSTLTLQPYMRQFVAHL 780  
Qy 781 QETSPRLDAVIEOSSLINEASSGLFDVFLRPMCHAVRIRGKSVQCQIPQSGIISLTL 840  
Db 781 QETSPRLDAVIEOSSLINEASSGLFDVFLRPMCHAVRIRGKSVQCQIPQSGIISLTL 840  
Qy 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900  
Db 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900  
Qy 901 RKTVVNPFVEALGGTAFVQMPAHGLPPWCGLLLDTRTLEVSQDSYSSYARTSRASLTF 960  
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Db 961 NRGFKAGNMRKLPVLRKCHSLFDLQVNSLQTVCTNLYKILLQAVFHCVLQLP 1020  
Qy 1021 FHQQWKNPTEFLRVIDSTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080  
Db 1021 FHQQWKNPTEFLRVIDSTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080  
Qy 1081 KLTRHRTVYVPLGSLRTAQQLSRKLPGTTLTALAANPALPSDFKTILD 1132  
Db 1081 KLTRHRTVYVPLGSLRTAQQLSRKLPGTTLTALAANPALPSDFKTILD 1132

RESULT 11

US-09-953-052-2  
; Sequence 2, Application US/09953052  
; Patent No. 6627619

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.

TITLE OF INVENTION: Antisense Compositions for Detecting and  
; Inhibiting Telomerase Reverse Transcriptase

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/953,052  
; FILING DATE: 14-Sep-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/052,919  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/974,549  
FILING DATE: 19-NOV-1997  
APPLICATION NUMBER: US 08/974,584  
FILING DATE: 19-NOV-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Parent, Annette S.  
REGISTRATION NUMBER: 42,058  
REFERENCE/DOCKET NUMBER: 015389-0036000US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1132 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-953-052-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 301 ROHHAGPPSTSRPPRPWDTECPVYAEKHLFVSSGDKBQLRPSFLSSLRPSLTGARRL 360  
Db 301 ROHHAGPPSTSRPPRPWDTECPVYAEKHLFVSSGDKBQLRPSFLSSLRPSLTGARRL 360  
Qy 361 VETIFLGSRRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPCYVLLKTHCPLRAVT 420  
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Db 421 PAAGVCAREKPGQSVAAPEEDTDPRLVQLLRQHSPPQVYGFVRACLRLVPPGLWGS 480  
Qy 481 RHNERFLRNTKKFISLGKHAKLSLOBLTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540  
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RESULT 12

US-09-042-460-3  
; Sequence 3, Application US/09042460  
; Patent No. 6767719

GENERAL INFORMATION:

; APPLICANT: Morin, Gregg B.  
; APPLICANT: Allsopp, Richard  
; APPLICANT: Depinho, Ronald  
; APPLICANT: Greenberg, Roger  
; TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patencin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042,460

; FILING DATE: 16-MAR-1998  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; PRIOR APPLICATION DATA: US 08/844,419  
; FILING DATE: 18-APR-1997  
; PRIOR APPLICATION DATA: US 08/846,017  
; FILING DATE: 25-APR-1997  
; PRIOR APPLICATION DATA: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; PRIOR APPLICATION DATA: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; PRIOR APPLICATION DATA: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; PRIOR APPLICATION DATA: US 08/974,549  
; FILING DATE: 19-NOV-1997  
; PRIOR APPLICATION DATA: US 08/974,584  
; FILING DATE: 19-NOV-1997  
; PRIOR APPLICATION DATA: US 08/979,742  
; FILING DATE: 26-NOV-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Einhorn, Gregory P.  
; REGISTRATION NUMBER: 38,440  
; REFERENCE/DOCKET NUMBER: 015389-003110US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1132 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..1132  
; OTHER INFORMATION: /note= "human telomerase reverse  
; OTHER INFORMATION: transcriptase (hTRT)"  
US-09-042-460-3

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MPRAFCRAVRSLLRSHRYEVLPLATFVRRLPGQGWRLVQRGDPAAFRALVAQCLVCVPW 60  
Qy 61 DARPPPAAPSPFQVSCCLKELVARLQRLCERGAKNVLAFAFGFALLDGCARGGPPPEAFTTSVR 120  
Db 61 DARPPPAAPSPFQVSCCLKELVARLQRLCERGAKNVLAFAFGFALLDGCARGGPPPEAFTTSVR 120



LOCATION: 1..1154  
OTHER INFORMATION: /notes="fusion protein composed of hTERT  
OTHER INFORMATION: protein sequence, vector sequences, the  
OTHER INFORMATION: Myc epitope and His6 tag"  
US-08-974-549A-611

Query Match 100.0%; Score 5961; DB 3; Length 1154;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVSLRSHREVLPATFVRRLLPQGNRLVQRGDPAAPALVAQCLVCPV 60  
Db 1 MPAPRCRAVSLRSHREVLPATFVRRLLPQGNRLVQRGDPAAPALVAQCLVCPV 60

QY 61 DARPPPAAPSRQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGAGGPEAFTTSVR 120  
Db 61 DARPPPAAPSRQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGAGGPEAFTTSVR 120

QY 121 SYLPTNTVDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180  
Db 121 SYLPTNTVDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATOARPPPHASRRRLGCEAWNHSVREAGVPLGLPAGARRRGGSASRLPLPKPRR 240  
Db 181 ATOARPPPHASRRRLGCEAWNHSVREAGVPLGLPAGARRRGGSASRLPLPKPRR 240

QY 241 GAAPEPERTVQGSWAHPGRTGRPSDRGFCVSPARPAEATSLEGALSSTRHSHPSVG 300  
Db 241 GAAPEPERTVQGSWAHPGRTGRPSDRGFCVSPARPAEATSLEGALSSTRHSHPSVG 300

QY 301 ROHAGAPPSTSRPPMDTPCPVYAEKTHFLYSSGDKQLRPSFLSLRPSLTGARRL 360  
Db 301 ROHAGAPPSTSRPPMDTPCPVYAEKTHFLYSSGDKQLRPSFLSLRPSLTGARRL 360

QY 361 VETIFLGSRRPMCTPRRLPRLPORYWQMRPLELILGNHAQCPYGVLLKTHCPRAAVT 420  
Db 361 VETIFLGSRRPMCTPRRLPRLPORYWQMRPLELILGNHAQCPYGVLLKTHCPRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSHPWQVYGFVRACLRLVPPGLWGS 480  
Db 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSHPWQVYGFVRACLRLVPPGLWGS 480

QY 481 RHNERRLRNTKFIISLGKAKLSQLBLTWKMSVRDCAWLRRSPGVCGVPAABHRLREEI 540  
Db 481 RHNERRLRNTKFIISLGKAKLSQLBLTWKMSVRDCAWLRRSPGVCGVPAABHRLREEI 540

QY 541 LAKEFLHLMSSVYVELLSRFFYVTTTFQKNRFFFYRKSVWSKLQSIGIRQHLKRVOLRE 600  
Db 541 LAKEFLHLMSSVYVELLSRFFYVTTTFQKNRFFFYRKSVWSKLQSIGIRQHLKRVOLRE 600

QY 601 LSEAEVQRHREARPAALTSRLRFPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660  
Db 601 LSEAEVQRHREARPAALTSRLRFPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660

QY 661 LFSVLNVERARRCLLGASVLGLDDTHRAWRTFVLVRAQDPPPELYFKVDVTGAYDTI 720  
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QY 781 QETSPLRDVAIVIQSSSLNEASSGLFDVFLRFMFCHAVRIRGKSVYQCQGI PQGSILSTL 840  
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QY 841 LCSLCYGDMEKLFAGIRDGGLLRVDDFLVTPHLLTHAKTFLRLVRGVEYGCNVNL 900  
Db 841 LCSLCYGDMEKLFAGIRDGGLLRVDDFLVTPHLLTHAKTFLRLVRGVEYGCNVNL 900

QY 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSVARTSIRASLTF 960  
Db 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSVARTSIRASLTF 960

QY 961 NRGFKAGNNRRKLFGLVRLKCHSLFLDLQVNSLQVCTNYYKILLQAYRPHACVLQLP 1020  
Db 961 NRGFKAGNNRRKLFGLVRLKCHSLFLDLQVNSLQVCTNYYKILLQAYRPHACVLQLP 1020

QY 1021 FHOQVKNPTFFFLRVLSDTASLCYSTILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080  
Db 1021 FHOQVKNPTFFFLRVLSDTASLCYSTILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080

QY 1081 KLTHRVTVYVPLGLSLRTAQTLQSRKLPDGTTLTALAAAAANPALPSDFKTILD 1132  
Db 1081 KLTHRVTVYVPLGLSLRTAQTLQSRKLPDGTTLTALAAAAANPALPSDFKTILD 1132

RESULT 14  
US-08-912-951-323  
; Sequence 323, Application US/08912951  
; Patent No. 6475789  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
; NUMBER OF SEQUENCES: 335  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,951  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002600US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 323:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
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; US-08-912-951-323

Query Match      100.0%; Score 5961; DB 4; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLSRSHYREVLPLATFVRRLPGQWRLVQRGDPAAPRALVAQCVCVWP 60
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Qy 481 RHNERRFLRNTKFIISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCPVAAEHLRBEI 540
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RESULT 15

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US-09-402-181B-611
; Sequence 611, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;             Lingner, Joachim
;             Nakamura, Toru
;             Chapman, Karen B.
;             Morin, Gregg B.
;             Harley, Calvin B.
;             Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402.181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 611:
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SEQUENCE CHARACTERISTICS:  
LENGTH: 1154 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..1154  
OTHER INFORMATION: /notes "fusion protein composed of htrr  
protein sequence, vector sequences, the  
Myc epitope and His6 tag"  
SEQUENCE DESCRIPTION: SEQ ID NO: 611:  
US-09-402-181B-611

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Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Job time : 47 secs